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OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 01:03:53 ; Search time 323.574 Seconds
(without alignments)
4675.326 Million cell updates/sec

Title: US-10-734-373-59
Perfect score: 690
Sequence: 1 atggattccacactgtgtc.....gaacaattgagccagaagtt 690

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 14437070

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Result No.	Score	Query Match	ID	Description
1	38.8	5.6	528	US-09-925-065A-597659 Sequence 597659,
2	35.8	5.2	2427	US-09-925-065A-704634 Sequence 704634,
3	35.6	5.2	8196	US-10-678-790-53 Sequence 53, Appl
4	35.4	5.1	576	US-09-925-065A-408802 Sequence 408802,
5	35.4	5.1	1576	US-09-925-065A-408803 Sequence 408803,
6	35.2	5.1	1576	US-10-973-115B-301 Sequence 301, App
7	35.2	5.1	1263	US-10-131-826A-301 Sequence 301, App
8	35.2	5.1	2263	US-11-245-147-87 Sequence 87, Appl
9	34	4.9	615	US-09-925-065A-768990 Sequence 768990,
10	33.8	4.9	522	US-09-925-065A-316303 Sequence 316303,
11	33.8	4.9	598	US-09-925-065A-621004 Sequence 621004,
12	33.6	4.9	576	US-09-925-065A-332454 Sequence 332454,
13	33.2	4.8	583	US-09-925-065A-329025 Sequence 329025,
14	33.2	4.8	607	US-09-925-065A-470072 Sequence 470072,
15	33.2	4.8	629	US-09-925-065A-782109 Sequence 782109,
16	33.2	4.8	629	US-09-925-065A-843006 Sequence 843006,
17	33.2	4.8	630	US-09-925-065A-794377 Sequence 794377,
18	33.2	4.8	630	US-09-925-065A-850295 Sequence 850295,
19	33.2	4.8	978	US-09-925-065A-288846 Sequence 288846,
20	33.2	4.8	1357	US-10-750-185-47484 Sequence 47484, A

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Database : Published Applications NA New:*

- 1: /cgn2_6/ptodata/1/pubpna/US06 NEW PUB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US06 NEW PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US07 NEW PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US09 NEW PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/US10 NEW PUB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US10 NEW PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US10 NEW PUB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US11 NEW PUB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11 NEW PUB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US11 NEW PUB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US11 NEW PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US60 NEW PUB.seq.*

ALIGNMENTS

RESULT 1

US-09-925-065A-597659
; Sequence 597659, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108627.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 597659
; LENGTH: 528
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-925-065A-597659

Query Match 5.6%; Score 38.8; DB 6; Length 528;
Best Local Similarity 49.0%; Pred. No. 0.17;
Matches 103; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY	10	AACACTGTGTCAAGCTTTCAGGTAGACTGTTTCTTTGGCATGTCCGCAACGATTTCGA	69
DB	255	ACCACCTGAGTCAACTATATTTCCAAACAAATCTCGGAGATAAGCTTCAGAAATACACA	314
QY	70	GACCAAGACTGGGTGATGCCCATTCCTTGTGCGGCTTCGCGAGCAGAGTCCCTTA	129
DB	315	GATTAAGAATGGGGCTCCCGCCAAACACCTTCCCTACCCACACGCTCTGCTC	374
QY	130	AAAGGAAGAGGTAGACTCTTGTGTCATGGAACAGCCACTGTGTCAGGAAGCAG	189

Wed Mar 8 09:11:20 2006

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; ORGANISM: mouse
; US-10-678-790-53

Query Match
Best Local Similarity 5.2%; Score 35.6; DB 8; Length 8196;
Matches 101; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 106 CTTCCGCCAGACCCAGAAAGTCCCTTAAAGGAAGAGGTAGGACTCTTGGTCTGGACATCGAA 165
Db 4213 CATGCCAAGAGAGAGATAAAGGAGAAAGGAGAGAGAAATAAAGGCTAGAGACTAAGAA 4154
QY 166 ACAGCCACTCTGTCAGGAGAGATAGTGGAGAGAGTCTCGAAGAGGAATCAGATGAG 225
Db 4153 AGCTTAAAGAGAGAGAGGTAAGCTTAGAGAGATAGAGATAGAGATAGAGTAAAGGGAGAGT 4094
QY 226 GCATTTAAATAGACCATTCCTCTGTTCTGCTTCTTCAAGCTTAACTTACATGACTCTT 285
Db 4093 GAGGTGGGCCCAACAGCCCCCTTGTATCTGTTCTAGGTAACTGGGAGAGTCTA 4034
QY 286 GATGAGATCTCAAGAGAGACTGGTTCATGCTC 315
Db 4033 GCCTAAAGGGCAGAAAGCTTGGGGCATTGTC 4004

RESULT 4
US-09-925-065A-408802
; Sequence 408802, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 408802
; LENGTH: 576
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-408802

Query Match
Best Local Similarity 5.1%; Score 35.4; DB 6; Length 576;
Matches 57; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 464 CAGTCTGGCGAAATTTCCACCATTCCTCTTCCAGGACATATAATGAGGATCTCA 523
Db 425 CAGGCTTTGCAAGCTTTACCTCTCTCTTCCAGGACTCAGATGAAAGAAA 484
QY 524 AAANTGCAATTTGGGCTCTCATCGGAGACTTA 556
Db 485 TAAATGCAAGTAAGCTCAICGGTGTCTCA 517

RESULT 5
US-09-925-065A-408803
; Sequence 408803, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; US-10-678-790-53/c
; Sequence 53, Application US/10678790
; Publication No. US20050287530A1
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; TITLE OF INVENTION: TCL-1b Gene and Protein and Related Methods and
; FILE REFERENCE: CRO01.NP003
; CURRENT APPLICATION NUMBER: US/10/678,790
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US/09/526,329
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: PROVISION 60/124,714
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 8196
; TYPE: DNA
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; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 301
; LENGTH: 1576
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-826A-301

Query Match
Best Local Similarity 5.1%; Score 35.2; DB 8; Length 1576;
Matches 91; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 344 TATGTATAGAAATGGACAGGCAATCATGGATAAGACATCATCTACTTAAAGCAACTTTA 403
DB 1032 TTGTGCGAAGTATTTTCGGGTATAGAGAAATTTGAATTTTCTTAAGACAGATACAT 973
QY 404 GTGTGATTTTGAAGGCTGGAGACACTAATACTACTTGTAGAGCCTTCCCGAGAGGAG 463
DB 972 AAGTGAAGAAGCAACACAGGAGGCATTGATTTCTTACTCGAGGTTGAGCTG 913
QY 464 CAGTCGTGCGCAATTTCCACCATTCCTCTCTTCCAGACATATAATAGGAGATGCA 523
DB 912 CATTAGTTTTCCATTTGGCAAGATTTTGTCTTTTAGCAGAGAATCATGAAGATAATT 853
QY 524 AAAA 527
DB 852 ATAA 849

RESULT 8
US-11-245-147-87/C
; Sequence 87, Application US/11245147
; Publication No. US20060030541A1
; GENERAL INFORMATION:
; APPLICANT: GARCIA, TERESA
; APPLICANT: ROMAN ROMAN, SERGIO
; APPLICANT: BARON, ROLAND
; APPLICANT: CALL, KATHERINE
; APPLICANT: THEILHABER, JOACHIM
; APPLICANT: CONNOLLY, TIMOTHY
; APPLICANT: JACKSON, AMANDA
; APPLICANT: BUSHNELL, STEVEN
; APPLICANT: RANADI, GEORGES
; TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE
; FILE REFERENCE: 37991-0023
; CURRENT APPLICATION NUMBER: US/11/245,147
; PRIOR FILING DATE: 2005-10-07
; PRIOR APPLICATION NUMBER: PCT/IB02/02211
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/281,400
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 87
; LENGTH: 2263
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-245-147-87

Query Match
Best Local Similarity 5.1%; Score 35.2; DB 9; Length 2263;
Matches 91; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 344 TATGTATAGAAATGGACAGGCAATCATGGATAAGACATCATCTACTTAAAGCAACTTTA 403
DB 865 TTGTGCGAAGTATTTTCGGGTATAGAGAAATTTGAATTTTCTTAAGACAGATACAT 806
QY 404 GTGTGATTTTGAAGGCTGGAGACACTAATACTACTTGTAGAGCCTTCCCGAGAGGAG 463
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DB 805 AAGTGAAGAAGCAACACAGGAGGCATTGATTTCTTAATCTGTCTTACTCGAGAGTTGAGCTG 746
QY 464 CAGTCGTGCGCAAAATTTCCACCATTCCTCTTCCAGACATATAATAGGAGATGCA 523
DB 745 CATTAGTTTTCCATTTTGGCAAGATTTTGTCTTTTAGCAGAGAATCATGAAGATAATT 686
QY 524 AAAA 527
DB 685 ATAA 682

RESULT 9
US-09-925-065A-768990/C
; Sequence 768990, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 768990
; LENGTH: 615
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-768990

Query Match
Best Local Similarity 4.9%; Score 34; DB 6; Length 615;
Matches 55; Conservative 1; Mismatches 36; Indels 0; Gaps 0;

QY 175 CQTGCGAAGCAAGATGTGAGCAGATTCGGAAGAGCAATCAGATGAGGCACTAAA 234
DB 429 CTCGAGATATCAGCCAGATGTGAAGTTTATCCAGTACTTTAGAGAGGAGAACTAAA 370
QY 235 ATGACCATTCCTCTGCTTCCTTCAGCTA 266
DB 369 ATCAGAAATGCTATGTTCAATTTCYCCTA 338

RESULT 10
US-09-925-065A-316303
; Sequence 316303, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
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; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 316303
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-316303

Query Match      4.9%; Score 33.8; DB 6; Length 522;
Best Local Similarity 49.7%; Pred. No. 5.6;
Matches 83; Conservative 1; Mismatches 83; Indels 0; Gaps 0;

QY 350 TAAGATGGACCAAGCAATCATGGATAGACATCATCTTAAAGCAACTTTAGTGTGA 409
DB 211 TAATATCTGAAAGTAGTGTGAGGTTAAAGACATACATGTAAGATTGAAATTGGA 270
QY 410 TTTTCGAAGCTGGAGACACTAATCTACTTAGAGCCTTACCCAGAGAGCAGCTCG 469
DB 271 TTTTGAAGTCTGTCAATATCAAAAGTTTAAACACTTCTCGAATAGATGATCAAG 330
QY 470 TTGGGGAATTTCCACCATTCCTCTCTTCAGGACATCTAATGAG 516
DB 331 TCATTGTAAATATATAGTCATTATTATAGCAAGGCATATTGATCG 377

RESULT 11
US-09-925-065A-621004
; Sequence 621004, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 621004
; LENGTH: 598
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-621004

Query Match      4.9%; Score 33.8; DB 6; Length 598;
Best Local Similarity 50.3%; Pred. No. 5.9;
Matches 83; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 46 TGGCATGTCCGAAACGATTTGACAGACCAAGAACTGGGTGATGCCCATTCCTTGACCG 105
DB 42 TGAATGAATCAGAGAGGAGCAGATCCAGATAGGCGGCTTGTGATGGAAGG 101
QY 106 CTTCCGAGACCAAGATCCCTAAAGGAGAGGTAGCTCTGTGCTGACATCGAA 165
DB 102 CTTTGGGAGACCAATYTGGAATTTGACAGAGAGAACTGCTATGCTTGAATGTA 161
QY 166 ACAGCCACTGTCAGAGAAAGCAGATAGTGGAGCAGATCTTGAAA 210
DB 162 ACAGTTACTGTGCTCTGTGTGGAAATATAGTGGATGGGCAA 206
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RESULT 12
US-09-925-065A-332454/c
; Sequence 332454, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 332454
; LENGTH: 576
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-332454

Query Match      4.9%; Score 33.6; DB 6; Length 576;
Best Local Similarity 55.3%; Pred. No. 6.7;
Matches 63; Conservative 1; Mismatches 50; Indels 0; Gaps 0;

QY 338 GCTCCCTATGTATGAAGTATGACGAGCAATCATGGATAGACATCATCTTAAAGCAA 397
DB 335 GTTCTGTATTTAAAGTAAATCCAGAAATGATTAAGGCTAGCTATTATTATTCCA 276
QY 398 ACTTTAGTGTGATTTTCGAAGGCTGGAGACACTAATCTACTTAGAGCCTTCA 451
DB 275 AATTTTCAGTGAATCTTTAGAAATGCATCATGCTACTTTCTATTATGTTTA 222

RESULT 13
US-09-925-065A-329025
; Sequence 329025, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 329025
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-329025

Query Match      4.8%; Score 33.2; DB 6; Length 583;
Best Local Similarity 48.4%; Pred. No. 8.9;
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Matches 92; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 498 TCCAGGACATACATAGGATGTCACAAATGCAATTTGGGGTCTCTCATCGGAGACTTAA 557
Db 315 TCTAGAGCCACATACACAGAAATATAATATGCAATTCATAAAGAAAAAATGAACCTTA 374
QY 558 ATGGAAATGTAATACGGTTAGAACTCTGAACTCTACAGATTTCGGTGGAGAGCAG 617
Db 375 AIGTACCTAAATATATATGCAATATGTAACCTCYCAAAATAAGTGGGAGAAAAATG 434
QY 618 TCATCAGAAATGGGACCTTCATTCCTCCAAAGCAGAAACGAAAAATGGAGAGACAAT 677
Db 435 TGATGACAGATCTCAAAATCTGTTTCAGAAATCACTCAATAGCAAGAAAAAA 494
QY 678 TGAGCCAGAA 687
Db 495 ACAGTAAGAA 504

RESULT 14
US-09-925-065A-470072/c
; Sequence 470072, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 470072
; LENGTH: 607
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-470072

Query Match 4.8%; Score 33.2; DB 6; Length 607;
Best Local Similarity 51.3%; Pred. No. 9.1;
Matches 77; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 477 AATTTACCAATTCCTCTCTCCAGACATCTAATGAGATCTCAAAAATGCAATGG 536
Db 528 ATATGATGACATCTCTTGGCTCTCTAGGAACTAAAGTAAGATATAAATAGCCTTTA 469
QY 537 GGTCTCTATCGGAGACTTAATGATGTAATACGGTTAGATCTCTGAACTCTACA 596
Db 468 TGGCAGAAATCTAGGCAATTAAGAGAAATGAAGCAGAAAAACCTGCTTAGCTCTAAG 409
QY 597 GAGATTCGCTTGGAGAGCAGTCAATGAGAA 626
Db 408 AAGTCCTTTACAGAAAAACATATGATGGAA 379

RESULT 15
US-09-925-065A-782109/c
; Sequence 782109, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome

FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 782109
LENGTH: 629
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-782109

Query Match 4.8%; Score 33.2; DB 6; Length 629;
Best Local Similarity 49.4%; Pred. No. 9.3;
Matches 86; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 357 GGACCGCAATCATGATAGAACATCATCTTAAAGCAAACTTTAGTGTGATTTTGA 416
Db 483 GCAAAAGAGGAACATAAAGCATTAAACAATATTTAACTCAGCCATGAATAATATTATTA 424
QY 417 AAGGCTGGAGACACTAATCTACTTAGAGCCTTCACCGAAGAGGAGCAGTCTTGGCGA 476
Db 423 TACCATGATTAATGTTAATAGTACTAATGATTTAACAATAATTTATAAGGTAGTTGGGA 364
QY 477 AATTTACCAATTCCTCTCTCCAGACATCTAATGAGATCTCAAAAATGC 530
Db 363 AGTAAGAGAGTACAAAATCTCAAGGATAAAAAGGAATAAATAGATATATGC 310

Search completed: March 8, 2006, 01:39:34
Job time : 324.574 secs

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OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 00:04:28 ; Search time 4572.81 Seconds
(without alignments)
11038.514 Million cell updates/sec

Title: US-10-734-373-57
Perfect score: 888
Sequence: 1 agcaaaagcgggtgacaaa.....aaaaaacaccttcttcta 888

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pt.*
9: gb_pro.*
10: gb_sts.*
11: gb_sy.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	888	100.0	888	6	AR254669 Sequence
2	888	100.0	888	6	AR455544 Sequence
3	888	100.0	888	6	AX225029 Sequence
4	886.4	99.8	891	6	AR254664 Sequence
5	886.4	99.8	891	6	AR455539 Sequence
6	886.4	99.8	891	6	AX225022 Sequence
7	884.4	99.6	888	6	AR254666 Sequence
8	884.4	99.6	888	6	AR455541 Sequence
9	884.4	99.6	888	6	AX225025 Sequence
10	880	99.1	890	13	FLANSEQUTE
11	870.4	98.0	890	13	FLANSEQEN
12	868.8	97.8	890	13	FLANSEQON
13	868.8	97.8	890	13	FLANSEQUNM
14	867.2	97.7	890	13	FLANSEQNY
15	865.6	97.5	890	13	AY855345
16	865.6	97.5	890	13	FLANSEQCOR
17	865.6	97.5	890	13	FLANSEQSAN
18	857.6	96.6	890	13	FLANSEQFON

19	836.4	94.2	838	13	AF001666	AF001666	Influenza
20	834.8	94.0	838	13	AF001667	AF001667	Influenza
21	834.8	94.0	838	13	AF001668	AF001668	Influenza
22	834.8	94.0	838	13	AF001671	AF001671	Influenza
23	834.8	94.0	838	13	AF001673	AF001673	Influenza
24	831.5	93.6	838	13	AF001669	AF001669	Influenza
25	828.4	93.3	838	13	AF001664	AF001664	Influenza
26	825.2	92.9	838	13	AF001662	AF001662	Influenza
27	825.2	92.9	838	13	AF001670	AF001670	Influenza
28	810.8	91.3	838	13	AF001663	AF001663	Influenza
29	810.8	91.3	838	13	AF001672	AF001672	Influenza
30	807.6	90.9	838	13	AF001665	AF001665	Influenza
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32	793.6	89.4	890	13	FLANSWALNY	FLANSWALNY	Influenza A
33	788.8	88.8	890	13	IAU49486	IAU49486	Influenza A
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35	788.4	88.8	886	13	AY633120	AY633120	Influenza
36	785.6	88.5	890	13	AY650274	AY650274	Influenza
37	784	88.3	890	13	AY611528	AY611528	Influenza
38	784	88.3	890	13	AY646082	AY646082	Influenza
39	784	88.3	890	13	AY648291	AY648291	Influenza
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41	780.8	87.9	897	13	AY633328	AY633328	Influenza A
42	780.2	87.9	865	13	IAU85376	IAU85376	Influenza A
43	777.6	87.6	890	13	AF285889	AF285889	Influenza
44	777.6	87.6	890	13	FLANSSWCHI	FLANSSWCHI	Influenza A
45	777.6	87.6	890	13	INA410597	INA410597	Influenza

ALIGNMENTS

RESULT 1
AR254669 AR254669 888 bp DNA linear PAT 20-DEC-2002
LOCUS Sequence 57 from patent US 6482414.
DEFINITION
ACCESSION AR254669
VERSION AR254669.1 GI:27303690
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 888)
AUTHORS Dowling,P.W. and Youngner,J.S.
TITLE Cold-adapted equine influenza viruses
JOURNAL Patent: US 6482414-A 57 19-NOV-2002;
The University of Pittsburgh-of the Commonwealth System of Higher Education; Pittsburgh, PA

FEATURES
source
1..888
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match	100.0%;	Score 888;	DB 6;	Length 888;
Best Local Similarity	100.0%;	Pred. No. 2.8e-209;	Mismatches 0;	Indels 0;
Matches 888;	Conservative 0;	Gaps 0;		
QY	1	AGCAAAAGCAGGTCACAAAACATAATCGATTCCACACTGTGTCAAGCTTTCAGGTAG	60	
Db	1	AGCAAAAGCAGGTCACAAAACATAATCGATTCCACACTGTGTCAAGCTTTCAGGTAG	60	
QY	61	ACTGTTTCTTGGCGATTCGCAACAGATTGGAGCACCAGACTGGGTGATGCCCAT	120	
Db	61	ACTGTTTCTTGGCGATTCGCAACAGATTGGAGCACCAGACTGGGTGATGCCCAT	120	
QY	121	TCCTTGACCGCTTCGCGGAGACAGAACTCCCTTAAAGGAGAGGTAGCTCTTGGTC	180	
Db	121	TCCTTGACCGCTTCGCGGAGACAGAACTCCCTTAAAGGAGAGGTAGCTCTTGGTC	180	
QY	181	TGCACATCGAAACAGCCACTCGTGCGAGGAAACAGATAGTGAGAGAGG	240	
Db	181	TGCACATCGAAACAGCCACTCGTGCGAGGAAACAGATAGTGAGAGAGG	240	

	Qy	241	AATCAGATGAGGCACCTTAAATGACCATTGCTTCGTCTCGCTTCAAGCTACTTAACCTG	300
	Dd	241	AATCAGATGAGGCACCTTAAATGACCATTGCTTCGTCTCGCTTCAAGCTACTTAACCTG	300
	Qy	301	ACATGACTCTTGATGAGATGCTCAAGAGACTGGTTTCACTGCTCATGCCAAGCAGAAGTAA	360
	Dd	301	ACATGACTCTTGATGAGATGCTCAAGAGACTGGTTTCACTGCTCATGCCAAGCAGAAGTAA	360
	Qy	361	CAGGCTCCCTAATGATAAGATGGGCAAGGCATCATGGAATAAGAACATCATACTTTAAG	420
	Dd	361	CAGGCTCCCTAATGATAAGATGGGCAAGGCATCATGGAATAAGAACATCATACTTTAAG	420
	Qy	421	CAAACCTTTAGTGTGATTTCCGAAGGCTGGAGACAATAATACTACTTAGAGCTTCCACG	480
	Dd	421	CAAACCTTTAGTGTGATTTCCGAAGGCTGGAGACAATAATACTACTTAGAGCTTCCACG	480
	Qy	481	AGAAGAAGGACGAGTCGTTGGCGAAAATTTCAACATTTGCTCTTCCAGGACATCTAATG	540
	Dd	481	AGAAGAAGGACGAGTCGTTGGCGAAAATTTCAACATTTGCTCTTCCAGGACATCTAATG	540
	Qy	541	AGGATGTCAAAAATGCAATTTGGGGTCTCATCGAGAGACTTAAATGGAATGATATACGG	600
	Dd	541	AGGATGTCAAAAATGCAATTTGGGGTCTCATCGAGAGACTTAAATGGAATGATATACGG	600
	Qy	601	TTAGAATCTCTGAAACTCTACAGAGATTCGCTTGGAGAGCACTCATGAGAATGGGAGAC	660
	Dd	601	TTAGAATCTCTGAAACTCTACAGAGATTCGCTTGGAGAGCACTCATGAGAATGGGAGAC	660
	Qy	661	CTTCATTCCTCCAAAGCAGAAACGAAAAATGGAGAGAACTTGGAGCAGAGCTTTGAA	720
	Dd	661	CTTCATTCCTCCAAAGCAGAAACGAAAAATGGAGAGAACTTGGAGCAGAGCTTTGAA	720
	Qy	721	GAAATGAAGATGGTTGATTTGAAGAAGTGGCACATAGATTGAAAAATACAGAAATAGTTTT	780
	Dd	721	GAAATGAAGATGGTTGATTTGAAGAAGTGGCACATAGATTGAAAAATACAGAAATAGTTTT	780
	Qy	781	GAACAATTAACATTTATTCGAGCCTTACAACTATTGCTTGAAGTACAGACAGATAAGA	840
	Dd	781	GAACAATTAACATTTATTCGAGCCTTACAACTATTGCTTGAAGTACAGACAGATAAGA	840
	Qy	841	ACTTCTCGTTTCAGCTATTATATGATCAATAAAACACCCCTTGTTCTA	888
	Dd	841	ACTTCTCGTTTCAGCTATTATATGATCAATAAAACACCCCTTGTTCTA	888
RESULT 2				PAT 20-FEB-2004
AR455544	LOCUS		888 bp	DNA
DEFINITION		Sequence 57 from patent US 6685946.		
ACCESSION		AR455544		
VERSION		AR455544.1		
KEYWORDS		GI:42690364		
SOURCE		Unknown.		
ORGANISM		Unclassified.		
REFERENCE		1 (bases 1 to 888)		
AUTHORS		Dowling,P.W. and Youngner,J.S.		
TITLE		Cold-adapted equine influenza viruses		
JOURNAL		Patent: US 6685946-A 57 03-FEB-2004;		
		The University of Pittsburgh-of the Commonwealth System of Higher Education; Pittsburgh, PA		
FEATURES		Location/Qualifiers		
source		1..888		
		/organism="unknown"		
		/mol_type="genomic DNA"		
ORIGIN				
Query Match		100.0%; Score 888; DB 6; Length 888;		
Best Local Similarity		100.0%; Pred. No. 2..8e-209;		
Matches 888; Conservative		0; Mismatches 0; Indels 0; Gaps 0;		
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Db 481 AAGAAGGAGCAGTGGTGGGAAAATTTCCAAATTCGCTTCTCTCCAGCAGATTAATG 540
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Db 541 AGGATGTCAAAATATGCAATTTGGGTCCTTCAGGAGCATTAATAATGGAATGATAATACGG 600
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Qy 661 CTTCAATTCCTCCAAAGCAGAAAACGAAAATGGAGAGAACAAATGAGCCAGAGTTGAA 720
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Qy 840 GAAATAGAGTGGTGGATTTGAAGAGTGGAGATGAGATGAGAAAATACAGAAATAGTTTT 840
Db 840 GAAATAGAGTGGTGGATTTGAAGAGTGGAGATGAGATGAGAAAATACAGAAATAGTTTT 840
Qy 841 ACTTCTCGTTTCAGCTTATTAATGATATAAAACACCCCTTGTCTTA 888
Db 841 ACTTCTCGTTTCAGCTTATTAATGATATAAAACACCCCTTGTCTTA 888

RESULT 5
AR455539 891 bp DNA linear PAT 20-FEB-2004
LOCUS Sequence 50 from patent US 6685946.
DEFINITION AR455539
ACCESSION AR455539.1 GI:42690359
VERSION
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 891)
AUTHORS Dowling, P.W. and Youngner, J.S.
TITLE Cold-adapted equine influenza viruses
JOURNAL Patent: US 6685946-A 50 03-FEB-2004;
The University of Pittsburgh-of the Commonwealth System of Higher Education: Pittsburgh, PA
FEATURES
source Location/Qualifiers
1
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 99.8%; Score 886.4; DB 6; Length 891;
Best Local Similarity 99.9%; Pred No. 6,9e-209;
Matches 887; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 AGCAAGCAGGCTGACAAACATATGATTCACACCTGTGTCAGCTTTTCAGGTAG 60
Db 1 AGCAAGCAGGCTGACAAACATATGATTCACACCTGTGTCAGCTTTTCAGGTAG 60
Qy 61 ACTGTTTCTTGGCATGTCGCAACGATTCGACCAAGCACTGGGTGATGCCCAT 120
Db 61 ACTGTTTCTTGGCATGTCGCAACGATTCGACCAAGCACTGGGTGATGCCCAT 120
Qy 121 TCCTTGACCGGCTTCGCGAGCAGAGTCCCTTAAGAGAGAGGTAGCACTTGTGTC 180
Db 121 TCCTTGACCGGCTTCGCGAGCAGAGTCCCTTAAGAGAGAGGTAGCACTTGTGTC 180
Qy 181 TGACATCGAAACAGCAGCTCTGTCGAGGAGAGAGATGAGTGGAGAGG 240
Db 181 TGACATCGAAACAGCAGCTCTGTCGAGGAGAGAGATGAGTGGAGAGG 240
Qy 241 AATCAGATGAGGCTTAAATATGACATTCGCTTCTGCTTCAAGCTTAACTG 300
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Qy 361 CAGGCTCCCTATGATTAAGAAATGGACCAAGCAATCATGAGTAAGAAACATCATCTTAAG 420
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Db 781 GAAATAGAGTGGTGGATTTGAAGAGTGGAGATGAGATGAGAAAATACAGAAATAGTTTT 840
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Db 841 ACTTCTCGTTTCAGCTTATTAATGATATAAAACACCCCTTGTCTTA 888

RESULT 6
AX225022 891 bp DNA linear PAT 10-SEP-2001
LOCUS Sequence 32 from Patent WO0160849.
DEFINITION AX225022
ACCESSION AX225022.1 GI:15555095
VERSION
KEYWORDS
SOURCE Equine influenza virus H3N8
ORGANISM Equine influenza virus H3N8
REFERENCE 1 Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenzavirus A.
AUTHORS Dowling, P.W. and Youngner, J.S.
TITLE Cold-adapted equine influenza viruses
JOURNAL Patent: WO 0160849-A 32 23-AUG-2001;
UNIV. OF PITTSBURGH OF THE COMMONWEALTH SYSTEM OF HIGHER EDUCATION (US)
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source Location/Qualifiers
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27.719
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ORIGIN

Query Match 99.8%; Score 886.4; DB 6; Length 891;
Best Local Similarity 99.9%; Pred. No. 6.9e-209;
Matches 887; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCAAAAGCAGGGTGCACAAAACATAATGATTCACACACTGTGTCAAGCTTTTCAGGTAG 60
DB 1 AGCAAAAGCAGGGTGCACAAAACATAATGATTCACACACTGTGTCAAGCTTTTCAGGTAG 60

QY 61 ACTGTTTCTTTGGCATGTCCGCAACAGATTTGCAGACCAAGACTGGGTGATGCCCAT 120
DB 61 ACTGTTTCTTTGGCATGTCCGCAACAGATTTGCAGACCAAGACTGGGTGATGCCCAT 120

QY 121 TCCTTGACCGGCTTCGCGAGACAGAGTCCCTAAAGAGAGAGTAGTACTCTTGGTC 180
DB 121 TCCTTGACCGGCTTCGCGAGACAGAGTCCCTAAAGAGAGAGTAGTACTCTTGGTC 180

QY 181 TGCAGATCGAAACAGCCACTCGTGCAGGAAGCAGATAGTGGAGCATCTTGGAGAGG 240
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DB 241 AATCAGATGAGCACTTAAATGACCAATTCCTCTGTTCTTCCCTTCAACGCTACTTAACTG 300

QY 301 ACATGACTCTTGGATGAGATGTCAAGAGACTGGTTCATGCTCATGCCCAAGCAGAGAAAGTAA 360
DB 301 ACATGACTCTTGGATGAGATGTCAAGAGACTGGTTCATGCTCATGCCCAAGCAGAGAAAGTAA 360

QY 361 CAGGCTCCCTATGTATAGAAATGCACAGCAATCATGAGTAAAGACATCATACTTAAAG 420
DB 361 CAGGCTCCCTATGTATAGAAATGCACAGCAATCATGAGTAAAGACATCATACTTAAAG 420

QY 421 CAACCTTTAGTGTGATTTTCCGAAGGCTCGACACACTAATACTACTAGAGCCTTCACCG 480
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DB 481 AAGAAGGAGCAGTGTGGCGAAATTCACCAATTCCTCTCTCCAGGACACTAATG 540

QY 541 AGATGTCAAAAATGCAATTTGGGGTCTCATCGAGAGACTTAAATGGAATGATATACGG 600
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QY 601 TTAGAATCTCTGAATCTCAGAGATTCGCTTGGAGAGCAGTCTATGAGAAATGGAGAC 660
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QY 721 GAAATGAAGTGTGATTTGAGAGAGTGCACATAGATTTGAAATATACAGAAATAGTTT 780
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QY 781 GAACAAATTAACATTTATGCAAGCTTTTAAATGATTAAGAAACACCTTGTCTTA 840
DB 781 GAACAAATTAACATTTATGCAAGCTTTTAAATGATTAAGAAACACCTTGTCTTA 840

QY 841 ACTTTCTCGTTTCAGCTTATTTAATGATTAAGAAACACCTTGTCTTA 888
DB 841 ACTTTCTCGTTTCAGCTTATTTAATGATTAAGAAACACCTTGTCTTA 888

RESULT 7

AR254666 LOCUS 888 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 53 from patent US 6482414.
ACCESSION AR254666
VERSION AR254666.1 GI:27303687

KEYWORDS

Source Unknown.

ORGANISM

Unknown.

REFERENCE

1 (bases 1 to 888)

Dowling P.W. and Youngner J.S.

Cold-adapted equine influenza viruses

Patent: US 6482414-A 53 19-NOV-2002;

The University of Pittsburgh-of the Commonwealth System of Higher

Education, Pittsburgh, PA

FEATURES

source

1..888

Location/Qualifiers

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 99.6%; Score 884.4; DB 6; Length 888;
Best Local Similarity 99.9%; Pred. No. 2.2e-208;
Matches 885; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 CAAAGCAGGGTGCACAAAACATAATGATTCACACACTGTGTCAAGCTTTTCAGGTAG 60

QY 63 TGTGTTCTTTGGCATGTCCGCAACAGATTTGCAGACCAAGACTGGGTGATGCCCATTC 122
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QY 123 CTTGACCGGCTTCGCGAGACAGAGTCCCTAAAGAGAGAGTAGTACTCTTGGTCG 182
DB 123 CTTGACCGGCTTCGCGAGACAGAGTCCCTAAAGAGAGAGTAGTACTCTTGGTCG 180

QY 183 GACATCGAAACAGCCACTCGTGCAGGAAGCAGATAGTGGAGCATCTTGGAGAGGAA 242
DB 183 GACATCGAAACAGCCACTCGTGCAGGAAGCAGATAGTGGAGCATCTTGGAGAGGAA 240

QY 243 TCAGATGAGGCACTTAAATGACCAATTCCTCTCTCTCCAGGACACTAATG 302
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QY 303 ATGACTCTTGGATGAGATGTCAAGAGACTGGTTCATGCTCATGCCCAAGCAGAGTAA 362
DB 303 ATGACTCTTGGATGAGATGTCAAGAGACTGGTTCATGCTCATGCCCAAGCAGAGTAA 360

QY 363 GGTCTCTCTATGATTAAGAAATGGACCAAGTCTGATGATTAAGAAATGATTAAGAA 422
DB 363 GGTCTCTCTATGATTAAGAAATGGACCAAGTCTGATGATTAAGAAATGATTAAGAA 420

QY 423 AACCTTTAGTGTGATTTTCCGAAGGCTGGAGACACTAATATCTTAGAGCCTTCAACGAA 482
DB 423 AACCTTTAGTGTGATTTTCCGAAGGCTGGAGACACTAATATCTTAGAGCCTTCAACGAA 480

QY 483 GAAAGAGCAGTCTGTTGGCGAAATTCACCAATTCCTCTCTCCAGGACACTAATAG 542
DB 483 GAAAGAGCAGTCTGTTGGCGAAATTCACCAATTCCTCTCTCCAGGACACTAATAG 540

QY 543 GATGTCAAAATATGCAATTTGGGGTCTCATCGGAGACTTAAATGGAATGATTAAGCTT 602
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DB 603 AGATCTCTGAACTCTCAGAGATTCGCTTGGAGAGCAGTCTATGAGATGGAGACT 660

QY 663 TCATTCCCTCCAAAGCAGAAACGAAATTCGAGAGACAAATTTGAGCCAGAGTTTGA 722
DB 663 TCATTCCCTCCAAAGCAGAAACGAAATTCGAGAGACAAATTTGAGCCAGAGTTTGA 720

QY 723 AATAGATGGTTCATTTGAAGAGTGGCGACATAGATTTGAAATATACAGAAATAGTTTGA 782
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Qy 843 TTCTCGTTTCAGCTTATTTAATGATATAAAACACCCCTTGTCTTA 888
Db 841 TTCTCGTTTCAGCTTATTTAATGATATAAAACACCCCTTGTCTTA 886

RESULT 8
AR455541
LOCUS AR455541 888 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 53 from patent US 6685946.
ACCESSION AR455541
VERSION AR455541.1 GI:42690361
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 888)
AUTHORS Dowling, P.W. and Youngner, J.S.
TITLE Cold-adapted equine influenza viruses
JOURNAL Patent: US 6685946-A 53 03-FEB-2004;
The University of Pittsburgh-of the Commonwealth System of Higher Education; Pittsburgh, PA

FEATURES
source Location/Qualifiers
1..888
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 99.6%; Score 884.4; DB 6; Length 888;
Best Local Similarity 99.9%; Pred. No. 2.2e-208;
Matches 885; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CAAAGCAGGGTGACAAAACATATGATTCACACTGTGTCAAGCTTTCAGGTAGAC 62
Db 1 CAAAGCAGGGTGACAAAACATGATGGATTCACACTGTGTCAAGCTTTCAGGTAGAC 60

Qy 63 TGTTCCTTTGGCATGTCCGCAACGATTTGCGACCAAGAACTGGGTGATGCCCATTC 122
Db 61 TGTTCCTTTGGCATGTCCGCAACGATTTGCGACCAAGAACTGGGTGATGCCCATTC 120

Qy 123 CTTGACCGGCTTCGCGAGACCAAGTCCCTAAAGAGGAGAGTGTAGTCTTGTGTCTG 182
Db 121 CTTGACCGGCTTCGCGAGACCAAGTCCCTAAAGAGGAGAGTGTAGTCTTGTGTCTG 180

Qy 183 GACATCGAAGACGCACTTCGTGAGGAAAGCAGATAGTGGAGCAGATTTCTGGAAGAGAA 242
Db 181 GACATCGAAGACGCACTTCGTGAGGAAAGCAGATAGTGGAGCAGATTTCTGGAAGAGAA 240

Qy 243 TCAGATGAGGCACTTAATAGTACCTTCCTGCTTCAAGCTTCACTTAACTGAC 302
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Qy 303 ATGACTCTTGATGATGTCAAGAGCTGTTCATGCTCATGCCCGCAGAGAAAGTAACA 362
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Qy 363 GGCTCCCTATGATATAGATGGAACGAGGCTTCAGTATGAGACACTACTACTTAAAGCA 422
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Qy 723 AATAAGATGTTGATTGAAGAAAGTCGACATAGATTGAAAAATACAGAAAATAGTTTGA 782
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RESULT 9
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LOCUS AX225025 35 from Patent WO0160849.
DEFINITION Sequence 35 from Patent WO0160849.
ACCESSION AX225025
VERSION AX225025.1 GI:15555098
KEYWORDS Equine influenza virus H3N8
SOURCE Equine influenza virus H3N8
ORGANISM Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenzavirus A.

REFERENCE 1
AUTHORS Dowling, P.W. and Youngner, J.S.
TITLE Cold-adapted equine influenza viruses
JOURNAL Patent: WO 0160849-A 35 23-AUG-2001;
UNIV. OF PITTSBURGH OF THE COMMONWEALTH SYSTEM OF HIGHER EDUCATION (US)

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Best Local Similarity 99.9%; Pred. No. 2.2e-208;
Matches 885; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 QY 843 TTTCTCGTTTCAGCTTATTTAATGATAAAAAACCCCTTGTCTTA 888
 Db 841 TTTCTCGTTTCAGCTTATTTAATGATAAAAAACCCCTTGTCTTA 886

RESULT 10
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 LOCUS
 DEFINITION Influenza A virus isolate A/equine/Tennessee/5/86 nonstructural protein, complete cds. VRL 15-SEP-1998
 ACCESSION M80973
 VERSION M80973.1 GI:348780
 KEYWORDS
 SOURCE
 ORGANISM
 Influenza A virus
 Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 Influenzavirus A.
 1 (bases 1 to 890)
 Kawaoka, Y., Gorman, O.T., Ito, T., Wells, K., Denis, R.O.,
 Castucci, M.R., Donatelli, I., and Webster, R.G.
 Influence of host species on the evolution of the nonstructural
 (NS) gene of influenza A viruses
 JOURNAL Virus Res. 55 (2), 143-156 (1998)
 PUBMED 9725667
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ORIGIN
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 Db 61 ACTGTTTTCTTTGGCATGTCCGCAAAACGATTTTGCAGAACCTGGGTGATGCCCAT 120
 QY 121 TCCTTGACCGGCTTCGCCGAGACGAGAAGTCCCTTAAAGGAAGAGGTAGCACTCTTGGTC 180
 Db 121 TCCTTGACCGGCTTCGCCGAGACGAGAAGTCCCTTAAAGGAAGAGGTAGCACTCTTGGTC 180
 QY 181 TGGACATCGAAACAGCCACTCGTCAGAGAACGATAGTGGAGAGAGG 240
 Db 181 TGGACATCGAAACAGCCACTCGTCAGAGAACGATAGTGGAGAGAGG 240
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 Db 301 ACATGCTCTTGATGAGATGTCAAGAGACTGGTTCATGCTCATGCCCAAGCAGAAAGTAA 360
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 QY 841 ACTTCTCGTTTCAGCTTATTTAATGATAAAAAACCCCTTGTCTTA 888
 Db 841 ACTTCTCGTTTCAGCTTATTTAATGATAAAAAACCCCTTGTCTTA 888

RESULT 11
 FLANSEQUE
 LOCUS
 DEFINITION Influenza A virus isolate A/equine/Kentucky/76 nonstructural protein, complete cds. VRL 15-SEP-1998
 ACCESSION M80971
 VERSION M80971.1 GI:348780
 KEYWORDS
 SOURCE
 ORGANISM
 Influenza A virus
 Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 Influenzavirus A.
 1 (bases 1 to 890)
 Kawaoka, Y., Gorman, O.T., Ito, T., Wells, K., Denis, R.O.,
 Castucci, M.R., Donatelli, I., and Webster, R.G.
 Influence of host species on the evolution of the nonstructural
 (NS) gene of influenza A viruses
 JOURNAL Virus Res. 55 (2), 143-156 (1998)
 PUBMED 9725667
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FLANSEQUE
 LOCUS
 DEFINITION Influenza A virus isolate A/equine/Kentucky/76 nonstructural protein, complete cds. VRL 15-SEP-1998
 ACCESSION M80971

VERSION	M80971.1	GI:348768	
KEYWORDS	Influenza A virus		
SOURCE	Influenza A virus		
ORGANISM	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenzavirus A.		
REFERENCE	1 (bases 1 to 890)		
AUTHORS	Kawaoka,Y., Gorman,O.T., Ito,T., Wells,K., Donis,R.O., Castrucci,M.R., Donatelli,I. and Webster,R.G.		
TITLE	Influence of host species on the evolution of the nonstructural (NS) gene of influenza A viruses		
JOURNAL	Virus Res. 55 (2), 143-156 (1998)		
PUBMED	9725667		
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Query Match	98.0%;	Score 870.4;	DB 13; Length 890;
Best Local Similarity	98.8%;	Pred. No. 6.4e-205;	
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QY	61	ACTGTTTCTTGGATGTCGCGCAACGATTTTGCAGACCAAGAACTGGGGTATGCCCAT	120
DB	61	ACTGTTTCTTGGATGTCGCGCAACGATTTTGCAGACCAAGAACTGGGGTATGCCCAT	120
QY	121	TCCTTGACCGGCTTCGCCGAGCAGCAAGTCCCTAAAGGAAGAGGATGACACTCTTGGTC	180
DB	121	TCCTTGACCGGCTTCGCCGAGCAGCAAGTCCCTAAAGGAAGAGGATGACACTCTTGGTC	180
QY	181	TGGACATCGAAACAGCCACTCGTGCAGGAAAGCAGATAGTGGACGAGATTCGGAAGAGG	240
DB	181	TGGACATCGAAACAGCCACTCGTGCAGGAAAGCAGATAGTGGACGAGATTCGGAAGAGG	240
QY	241	AATCAGATGAGGCACCTTAAATGACCATTCCTCTCTTCTTCTTCTTCTTCTTCTTCTT	300
DB	241	AGTCAGATGAGGCACCTTAAATGACCATTCCTCTCTTCTTCTTCTTCTTCTTCTTCTT	300
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DB	661	CTTCAATTCCTCCAAAGCAGAAACGAAATATGGAGAGACATTCAGCCAGAAATTTGAA	720
QY	721	GAAATAAGATGTTGATTCGAAGATGGACATAGATTCGAAAATACAGAAATAGTTT	780
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QY	841	ACTTCTCTGTTTCAGCTTATTTAATGATAAAAAACACCTTGTCTTA	898
DB	841	ACTTCTCTGTTTCAGCTTATTTAATGATAAAAAACACCTTGTCTTA	898
RESULT 12			
FLANSEOLON			
LOCUS	FLANSEOLON	890 bp ss-RNA	linear VRL 15-SEP-1998
DEFINITION	Influenza A virus isolate A/equine/London/1417/73 nonstructural protein, complete cds.		
ACCESSION	M80954.1	GI:348770	
VERSION	M80954.1	GI:348770	
KEYWORDS	Influenza A virus		
SOURCE	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenzavirus A.		
ORGANISM	1 (bases 1 to 890)		
REFERENCE	Kawaoka,Y., Gorman,O.T., Ito,T., Wells,K., Donis,R.O., Castrucci,M.R., Donatelli,I. and Webster,R.G.		
AUTHORS	Influence of host species on the evolution of the nonstructural (NS) gene of influenza A viruses		
TITLE	Virus Res. 55 (2), 143-156 (1998)		
JOURNAL	9725667		
PUBMED	Location/Qualifiers		
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ORIGIN			
Query Match	97.8%;	Score 868.8;	DB 13; Length 890;
Best Local Similarity	98.6%;	Pred. No. 1.6e-204;	
Matches	876;	Conservative	0; Mismatches 12; Indels 0; Gaps 0;
QY	1	AGCAAAACAGAGGTCACAAAACATATGGATTCCAAACACTGTGTCAAGCTTTCAGGTAG	60
DB	1	AGCAAAACAGAGGTCACAAAACATATGGATTCCAAACACTGTGTCAAGCTTTCAGGTAG	60
QY	61	ACTGTTTCTTGGATGTCGCGCAACGATTTTGCAGACCAAGAACTGGGGTATGCCCAT	120
DB	61	ACTGTTTCTTGGATGTCGCGCAACGATTTTGCAGACCAAGAACTGGGGTATGCCCAT	120
QY	121	TCCTTGACCGGCTTCGCCGAGCAGCAAGTCCCTAAAGGAAGAGGATGACACTCTTGGTC	180

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RESULT 13

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PLANSEQNM 890 bp ss-RNA linear VRL 15-SEP-1998
LOCUS Influenza A virus isolate A/equine/New Market/79 nonstructural
DEFINITION protein, complete cds.
ACCESSION M80955
VERSION M80955.1 GI:348778
KEYWORDS Influenza A virus
SOURCE Influenza A virus
ORGANISM Influenza A virus
REFERENCE 1 (bases 1 to 890)
AUTHORS Kawaoka,Y., Gorman,O.T., Ito,T., Wells,K., Donis,R.O.,
Castrucci,M.R., Donatelli,I. and Webster,R.G.
TITLE Influence of host species on the evolution of the nonstructural
JOURNAL (NS) gene of influenza A viruses
PUBMED Virus Res. 55 (2), 143-156 (1998)
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KERNARTIESEV"
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ORIGIN

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Query Match 97.8%; Score 868.8; DB 13; Length 890;
Best Local Similarity 98.6%; Pred. No. 1.6e-204;
Matches 876; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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Db 1 AGCAAAAGCAGGCTGCAAAAACATAATCGATTCCACACCTGTCTCAAGCTTTCAGTAG 60
Qy 61 ACTGTTTCTTTGGCATGTCCGCAACAGATTTGAGACCAAGAACTGGGTGATGCCCAT 120
Db 61 ACTGTTTCTTTGGCATGTCCGCAACAGATTTGAGACCAAGAACTGGGTGATGCCCAT 120
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RESULT 14
FLANSEQNY
LOCUS
DEFINITION
Influenza A virus isolate A/equine/New York/49/73 nonstructural
protein, complete cds.
ACCESSION
M80976
VERSION
M80976.1
KEYWORDS
GI:348772
SOURCE
Influenza A virus
ORGANISM
Influenza A virus
Virus; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A.
1 (bases 1 to 890)
Kawaoka,Y., Gorman,O.T., Ito,T., Wells,K., Denis,R.O.,
Castrucci,M.R., Donatelli,I. and Webster,R.G.
Influence of host species on the evolution of the nonstructural
(NS) gene of influenza A viruses
Virus Res. 55 (2), 143-156 (1998)
PUBMED
9725667
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ORIGIN
Query Match 97.7%; Score 867.2; DB 13; Length 890;
Best Local Similarity 98.5%; Pred. No. 4e-204;
Matches 875; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
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RESULT 15
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protein gene, complete cds.
AY855345
AY855345.1 GI:60547114
Influenza A virus (A/equine/Kentucky/5/02 (H3N8))
Influenza A virus (A/equine/Kentucky/5/02 (H3N8))
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A.
1 (bases 1 to 890)
Quinlivan,M., Zamarin,D., Garcia-Sastre,A., Cullinane,A.,
Chambers,T. and Palese,P.
Attenuation of equine influenza viruses through truncations of the
NS1 protein
Unpublished
2 (bases 1 to 890)
Quinlivan,M., Zamarin,D., Garcia-Sastre,A., Cullinane,A.,
Chambers,T. and Palese,P.
Direct Submission
Submitted (14-DEC-2004) Microbiology, Mount Sinai School of
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ORIGIN
Query Match 97.5%; Score 865.6; DB 13; Length 890;
Best Local Similarity 98.4%; Fred. No. 9.9e-204;
Matches 874; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
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DB 121 TCCTTGACCGGCTTCGCGGAGACCAAGATCCCTAAAAGGAGAGGTATCACTCTTGGTC 180
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DB 241 AATCAGATAGGCACCTTAATATGACCATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
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QY 781 GAACAAAATAACATTTATGCAAGCCTTACAACTATTGCTTGAAGTAGAACCAAGAGATAAGA 840
DB 781 GAACAAAATAACATTTATGCAAGCCTTACAACTATTGCTTGAAGTAGAACCAAGAGATAAGA 840
QY 841 ACTTTCTCGTTTCAGCTTATTTAATGATAAAAAACACCCCTTGTGTTCTA 888

Db 841 ACTTTCTCGTTTCAGCTTATTTAATGATAAAAAACACCCCTTGTGTTCTA 888
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Job time : 4574.81 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 23:54:43 ; Search time 557.673 Seconds

(without alignments)
10612.397 Million cell updates/sec

Title: US-10-734-373-57

Perfect score: 888

Sequence: 1 agcaaaagcagggtgacaaa.....aaaaaacacctgtttcta 888

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: Geneseq1990s:*
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- 14: Geneseq2005bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	888	100.0	888	AAD15681	Aad15681 Equine in
2	886.4	99.8	891	AAD15678	Aad15678 Equine in
3	884.4	99.6	888	AAD15679	Aad15679 Equine in
4	744	83.8	890	AAX82197	Aax82197 Influenza
5	744	83.8	890	ADOL15247	Adol15247 Influenza
6	742.4	83.6	890	ADW44527	Adw44527 Influenza
7	737.6	83.1	890	AAD37061	Aad37061 Influenza
8	731.2	82.3	1146	3 AAD75003	Aad75003 Nucleotid
9	729.6	82.2	890	2 AAD22332	Aad22332 RNA (+),
10	707.2	79.6	890	6 ABA93942	Aba93942 Influenza
11	706.4	79.5	906	4 AAH77932	Aah77932 Nucleotid
12	692.8	78.0	824	14 ADY62118	Ady62118 Influenza
13	685	77.1	693	2 AAT37435	Aat37435 Non-struc
14	684.8	77.1	824	14 ADY62117	Ady62117 Influenza
15	463.4	52.2	468	4 AAD15680	Aad15680 Equine in
16	286.4	32.3	402	6 ABA93943	Aba93943 Influenza
17	213.4	24.0	6010	2 AAT59676	Aat59676 Plasmid P
18	213	24.0	696	2 AAD20237	Aad20237 Encodes V
19	212.8	24.0	918	2 AAD47361	Aad47361 Sequence

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22	212	23.9	453	2	AAT95097	Aat95097 Porcine s
23	212	23.9	453	6	AAD27035	Aad27035 Influenza
24	212	23.9	690	2	AAQ47362	Aaq47362 Sequence
25	212	23.9	690	2	AAQ70191	Aaq70191 Sequence
26	212	23.9	690	2	AAQ70209	Aaq70209 Sequence
27	212	23.9	524	2	AAQ40472	Aaq40472 Coding re
28	212	23.9	524	2	AAQ47364	Aaq47364 Sequence
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32	211.6	23.8	681	2	AAQ47369	Aaq47369 Sequence
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43	210.4	23.7	1020	2	AAQ38090	Aaq38090 NS1-ZQ1 f
44	210	23.6	729	2	AAQ47365	Aaq47365 Sequence
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ALIGNMENTS

RESULT 1

AAD15681

ID AAD15681 standard; DNA; 888 BP.

AC AAD15681;

DT 15-NOV-2001 (first entry)

DE Equine influenza virus H3N8 neicaiNS888 DNA.

XX Equine influenza virus; ei; cold adaptation; temperature sensitivity;

XX Equine influenza virus; ei; cold adaptation; temperature sensitivity;

XX Equine influenza virus H3N8 neicaiNS888 DNA; PeicaiNS230 protein; ds.

OS Equine influenza virus H3N8.

XX Key Location/Qualifiers

XX CDS 27..719

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FT /product= "PeicaiNS230 protein"

FT misc_feature 27..716

FT /*tag= b

FT /note= "This region is specifically claimed as SEQ ID NO: 41 in claim 2 of the specification"

FT

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XX WO200150849-A2.

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PT infections.

XX Claim 2; Page 75-76; 172pp; English.

CC The patent discloses cold-adapted equine influenza viruses and

CC reassortant influenza A viruses comprising at least one genome segment of

CC such an equine influenza virus, wherein the equine influenza virus genome

CC segment confers at least one identifying phenotype of the cold-adapted

CC equine influenza virus, such as cold adaptation, temperature sensitivity,

CC dominant interference or attenuation. The viruses are useful for

CC protecting animals from diseases caused by influenza viruses. They are

CC also used as vaccines. The present sequence is equine influenza (ei)

CC virus H3N8 neical (cold adapted) NS888 DNA encoding PeiwtINS230 protein

XX SQ Sequence 888 BP; 300 A; 173 C; 198 G; 217 T; 0 U; 0 Other;

Query Match 100.0%; Score 888; DB 4; Length 888;

Best Local Similarity 100.0%; Pred. No. 8.8e-239;

Matches 888; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 AGCAAAAGCAGGGTGACAAAACATATGGAATTCACACTGTGTCAAGCTTTCAGGTAG 60

QY 61 ACTGTTTTCTTTGGCATGTCGCAAAACGATTTGCAGACCAAGAACTGGGTGATGCCCAT 120

DB 61 ACTGTTTTCTTTGGCATGTCGCAAAACGATTTGCAGACCAAGAACTGGGTGATGCCCAT 120

QY 121 TCCTTGACCGGCTTCGCGGAGACAGAGAGTCCCTTAAAGGAAGAGGTAGCACTCTTGTC 180

DB 121 TCCTTGACCGGCTTCGCGGAGACAGAGAGTCCCTTAAAGGAAGAGGTAGCACTCTTGTC 180

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DB 181 TGGACATCGAAACAGCCACTCGTCAGGAAAGCAGATAGTGGAGCAGATTCGGAAGAGG 240

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QY 361 CAGGCTCCCTATGATAGATGAGATGGAGCAGGCAATCATGATAAGACATCATACTTAAAG 420

DB 361 CAGGCTCCCTATGATAGATGAGATGGAGCAGGCAATCATGATAAGACATCATACTTAAAG 420

QY 421 CAAACTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATACTTAGAGCCTTCACCG 480

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QY 481 AAGAAAGGACAGTCGTTGGCGAAATTTCAACATGCTTCTCCAGACATACTAATG 540

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QY 541 AGGATGTCAAAATGCAATTTGGGTCCTCATCGAGAGCTTAAATGGAATGATAACGG 600

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DB 661 CTTTCATTCCTCCAAAGCAGAAACGAAAAATGAGAGACATTTGGCCAGAGTTTGA 720

QY 721 GAAATAAGATGTTGATTTGAAGAGTGGCGACATAGATGAAATACAGAAATAGTTT 780

DB 721 GAAATAAGATGTTGATTTGAAGAGTGGCGACATAGATGAAATACAGAAATAGTTT 780

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RESULT 2

AD15678

ID AD15678 standard; DNA; 891 BP.

XX AC AD15678;

XX DT 15-NOV-2001 (first entry)

XX DE Equine influenza virus H3N8 neitwINS891 DNA.

XX KW Equine influenza virus; ei; cold adaptation; temperature sensitivity;

XX KW vaccine; neitwINS891 DNA; PeiwtINS230 protein; ds.

XX OS Equine influenza virus H3N8.

XX PH Key Location/Qualifiers

XX FI CDS 27..719

XX FI misc_feature 27..716

XX FI /tag= a

XX FI /product= "PeiwtINS230 protein"

XX FI /tag= b

XX FI /note= "This region specifically claimed as SEQ ID NO: 34 in claim 2 of the specification"

XX WO200160849-A2.

XX PD 23-AUG-2001.

XX PF 16-FEB-2001; 2001WO-US005048.

XX PR 16-FEB-2000; 2000US-00506286.

XX PA (UYP1-) UNIV PITTSBURGH.

XX PI Dowling PW, Youngner JS;

XX PI WPI; 2001-522584/57.

XX DR P-PSDB; AAE09027.

XX PT Novel isolated equine influenza virus (wild-type and cold-adapted) proteins and viruses containing nucleic acid molecules encoding the proteins, which are useful for protecting animals from influenza virus infections.

XX PS Claim 2; Page 71-72; 172pp; English.

XX CC The patent discloses cold-adapted equine influenza viruses and

XX CC reassortant influenza A viruses comprising at least one genome segment of

XX CC such an equine influenza virus, wherein the equine influenza virus genome

XX CC segment confers at least one identifying phenotype of the cold-adapted

XX CC equine influenza virus, such as cold adaptation, temperature sensitivity,

XX CC dominant interference or attenuation. The viruses are useful for

XX CC protecting animals from diseases caused by influenza viruses. They are

XX CC also used as vaccines. The present sequence is an equine influenza (ei)

XX CC virus H3N8 neitw1 (wild type) NS891 DNA encoding PeiwtINS230 protein

XX SQ Sequence 891 BP; 300 A; 174 C; 199 G; 218 T; 0 U; 0 Other;

Query Match 99.8%; Score 886.4; DB 4; Length 891;

Best Local Similarity 99.9%; Pred. No. 2.5e-238;

Matches 887; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 ACTGTTTCTTTGGCATGTCCGCAAAAGATTTGCGAGACCAAGAACTGGGTGATGCCCAT 120
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 QY 301 ACATGACTCTTGATGAGATGTCAGAGACTGCTCATGCTCATGCCCAAGCAGAACTAA 360
 Db 301 ACATGACTCTTGATGAGATGTCAGAGACTGCTCATGCTCATGCCCAAGCAGAACTAA 360
 QY 361 CAGGCTCCCTATGTATGAATGCGACCGCAATCATGGATAGACATCATACTTAAAG 420
 Db 361 CAGGCTCCCTATGTATGAATGCGACCGCAATCATGGATAGACATCATACTTAAAG 420
 QY 421 CAACCTTTAGTGTGATTTTCGAAGGCTGGAGACACTAATACTACTTAGAGCCTTCACCG 480
 Db 421 CAACCTTTAGTGTGATTTTCGAAGGCTGGAGACACTAATACTACTTAGAGCCTTCACCG 480
 QY 481 AAGAAGGAGCAGTCTGTTGGCGAAATTTCAACATTCGCTTCTTCCAGACATACTAATG 540
 Db 481 AAGAAGGAGCAGTCTGTTGGCGAAATTTCAACATTCGCTTCTTCCAGACATACTAATG 540
 QY 541 AGATGTCACAAAATGCAATTTGGGCTCTCATCGGAGACTTAAATGCAATGATTAATACGG 600
 Db 541 AGATGTCACAAAATGCAATTTGGGCTCTCATCGGAGACTTAAATGCAATGATTAATACGG 600
 QY 601 TTAGAATCTCTGAACCTCTACAGAGATTCGCTTGGAGAGCAGTCAATGAGATGGAGAC 660
 Db 601 TTAGAATCTCTGAACCTCTACAGAGATTCGCTTGGAGAGCAGTCAATGAGATGGAGAC 660
 QY 661 CTTTCATTCCTCCCAAGCAGACGAAATGGAGAGACAAATTTGAGCCAGCAAGTTTGA 720
 Db 661 CTTTCATTCCTCCCAAGCAGACGAAATGGAGAGACAAATTTGAGCCAGCAAGTTTGA 720
 QY 721 GAATAAGATGTTGATGAGAGTGGCACTAGATTTGAAAATACAGAAATAGTTTT 780
 Db 721 GAATAAGATGTTGATGAGAGTGGCACTAGATTTGAAAATACAGAAATAGTTTT 780
 QY 781 GAACAAATACATTTATGCAAGCCTTACACTATTGCTTGAAGTAGACAGAGATAAGA 840
 Db 781 GAACAAATACATTTATGCAAGCCTTACACTATTGCTTGAAGTAGACAGAGATAAGA 840
 QY 841 ACTTTCTGTTTCAGCTTATTTAATGATATAAAAAACCCCTTGTTTCTA 888
 Db 841 ACTTTCTGTTTCAGCTTATTTAATGATATAAAAAACCCCTTGTTTCTA 888

RESULT 3
 AAD15679
 ID AAD15679 standard; DNA; 888 bp.
 AC AAD15679;
 AC AAD15679;
 DT 15-NOV-2001 (first entry)
 DE Equine influenza virus H3N8 neiwt3NS888 DNA.
 DE Equine influenza virus; ei; cold adaptation; temperature sensitivity;
 KW vaccine; neiwt3NS888 DNA; ds.
 XX Equine influenza virus H3N8.
 OS Equine influenza virus H3N8.
 XX

PN WO200150849-A2.
 XX 23-AUG-2001.
 XX 16-FEB-2001; 2001WO-US005048.
 XX 16-FEB-2000; 2000US-00506286.
 XX (UYPI-) UNIV PITTSBURGH.
 XX Dowling PW, Youngner JS;
 XX WPI; 2001-522584/57.
 XX Novel isolated equine influenza virus (wild-type and cold-adapted)
 XX proteins and viruses containing nucleic acid molecules encoding the
 XX proteins, which are useful for protecting animals from influenza virus
 XX infections.
 XX Claim 2; Page 74; 172pp; English.
 XX The patent discloses cold-adapted equine influenza viruses and
 XX reasortant influenza A viruses comprising at least one genome segment of
 XX such an equine influenza virus, wherein the equine influenza virus genome
 XX segment confers at least one identifying phenotype of the cold-adapted
 XX equine influenza virus, such as cold adaptation, temperature sensitivity,
 XX dominant interference or attenuation. The viruses are useful for
 XX protecting animals from diseases caused by influenza viruses. They are
 XX also used as vaccines. The present sequence is an equine influenza (ei)
 XX virus H3N8 neiwt3 (wild type) NS888 DNA
 XX
 SQ Sequence 888 BP; 298 A; 174 C; 198 G; 218 T; 0 U; 0 Other;
 Query Match 99.6%; Score 884.4; DB 4; Length 888;
 Best Local Similarity 99.9%; Pred. No. 9e-238;
 Matches 885; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 CAAGAAGCGGTGACAAACATATGGAATTCACACCTGTGTCAAGCTTTCAGGTAGAC 62
 Db 1 CAAGAAGCGGTGACAAACATATGGAATTCACACCTGTGTCAAGCTTTCAGGTAGAC 60
 QY 63 TGTGTTCTTTGCACTGTCGCGAAGATTTGCGAGACCAAGCACTGGGTGATGCCCATTC 122
 Db 61 TGTGTTCTTTGCACTGTCGCGAAGATTTGCGAGACCAAGCACTGGGTGATGCCCATTC 120
 QY 123 CTTGACCGGCTTGGCCGAGACCAAGTCCCTAAAGGAAGAGTAGCACTCTTGCTG 182
 Db 121 CTTGACCGGCTTGGCCGAGACCAAGTCCCTAAAGGAAGAGTAGCACTCTTGCTG 180
 QY 183 GACATCGAAACAGCCACTCGTGCAGGAAAGCAGATAGTGGAGCAGATTTGGAAGAGAA 242
 Db 181 GACATCGAAACAGCCACTCGTGCAGGAAAGCAGATAGTGGAGCAGATTTGGAAGAGAA 240
 QY 243 TCAGATGAGGCACTTAAATGACCATTTGCTCTGTTCTGCTTCCAGCTACTTAACTGAC 302
 Db 241 TCAGATGAGGCACTTAAATGACCATTTGCTCTGTTCTGCTTCCAGCTACTTAACTGAC 300
 QY 303 ATGACTCTTGATGAGATGTCAGAGACTGTTTCATGCTCATGCCCAAGCAGAAAGTAACA 362
 Db 301 ATGACTCTTGATGAGATGTCAGAGACTGTTTCATGCTCATGCCCAAGCAGAAAGTAACA 360
 QY 363 GGCTCCCTATGTATGAAGATGGACCGCAATCATGGATAGACATCATACTTAAAGCA 422
 Db 361 GGCTCCCTATGTATGAAGATGGACCGCAATCATGGATAGACATCATACTTAAAGCA 420
 QY 423 AACTTTAGTGTGATTTTCGAAGGCTGGAGACACTAATACTACTTAGAGCCTTCACCGAA 482
 Db 421 AACTTTAGTGTGATTTTCGAAGGCTGGAGACACTAATACTACTTAGAGCCTTCACCGAA 480
 QY 483 GAAGAGAGCAGTCTGTTGGCGAAATTTCAACATTCGCTTCTTCCAGACATACTAATGAG 542
 Db 481 GAAGAGAGCAGTCTGTTGGCGAAATTTCAACATTCGCTTCTTCCAGACATACTAATGAG 540

QY 543 GATGTCATAAATCGATTCGGCTCTCATCGAGGACTTAAATGAATGATTAATACGGTT 602
DB 541 GATGTCATAAATCGATTCGGCTCTCATCGAGGACTTAAATGAATGATTAATACGGTT 600
QY 603 AGAATCTCTGAATCTACAGAGATTCCTTGGAGAGCAGTCATGAGATGGGAGACCT 662
DB 601 AGAATCTCTGAATCTACAGAGATTCCTTGGAGAGCAGTCATGAGATGGGAGACCT 660
QY 663 TCATTCCTCCAAAGCAGAAACGAAATATGAGAGAGACATTCGCGCAGATTTGAAGA 722
DB 661 TCATTCCTCCAAAGCAGAAACGAAATATGAGAGAGACATTCGCGCAGATTTGAAGA 720
QY 723 AATAAGATGGTTGATTCAAGAAGTGGCAGATAGATTTGAAATATGAGAAATAGTTTGA 782
DB 721 AATAAGATGGTTGATTCAAGAAGTGGCAGATAGATTTGAAATATGAGAAATAGTTTGA 780
QY 783 ACAAAATACATTTATGCAAGCCTTACAACTATTGCTTGAAGTAGAACCAAGAGATAAGAC 842
DB 781 ACAAAATACATTTATGCAAGCCTTACAACTATTGCTTGAAGTAGAACCAAGAGATAAGAC 840
QY 843 TTTCTCGTTTCAGCTTATTTAATGATAAAAAACACCCCTTGTCTTCTA 888
DB 841 TTTCTCGTTTCAGCTTATTTAATGATAAAAAACACCCCTTGTCTTCTA 886

RESULT 4

AX82197
ID AX82197 standard; DNA; 890 BP.
AC AX82197;
XX
XX
XX 18-AUG-1999 (first entry)
XX
XX Influenza virus NS protein gene sequence.
XX
XX Cold-adapted influenza virus; passage culture; PB1 protein; PB1 protein;
XX PA Protein; NP protein; M protein; NS protein; temperature sensitivity;
XX vaccine; flu; influenza; ss.
XX
XX Influenza virus.
XX
XX WO928445-A1.
XX
XX 10-JUN-1999.
XX
XX 30-NOV-1998; 98WO-KR000384.
XX
XX 29-NOV-1997; 97KR-00064854.
XX
XX (CHEI-) CHEIL JEDANG CORP.
XX
XX Seong BL, Lee KH, Yoon JW, Kim SJ, Cheoun KH, Kim J, Kim HG;
XX
XX WPI; 1999-385377/32.
XX
XX Cold-adapted influenza viruses useful for the production of protective
XX vaccines against flu.
XX
XX
XX Claim 4; Page 58; 62pp; English.

XX The invention relates to cold-adapted influenza viruses prepared by
XX passage culture of A/X-31, B/Yamagata/16/88 or B/Lee/40 viruses at low
XX temperatures. A cDNA gene of cold-adapted influenza virus H7N1-A101 can
XX be selected from a group consisting of PB2 protein gene, PB1 protein
XX gene, PA protein gene, NP protein gene, M protein gene and NS protein
XX gene (AX82192-X82197). The method is useful for the production of cold-
XX adapted influenza virus that exhibit temperature sensitivity and can be
XX actively grown in fertilized eggs. The virus is useful for vaccines for
XX protection against 'flu. Live vaccines containing cold-adapted viruses
XX have several advantages over killed vaccines. It can prevent reduction of
XX immunogenicity, which may occur in the killed vaccine where antigenic
XX proteins would be denatured at its inactivation. It can also avoid
XX hypersensitivity due to the prolonged administration of heterologous

CC proteins. It promotes the immunity by inducing IgA and it can be
CC administered into a spray formulation via nasal cavity and thus its
CC application is convenient for children. It is able to inhibit the growth
CC of the wild-type virus and thus its therapeutic effect can be expected.
CC The present sequence represents the influenza virus NS protein gene
XX
XX Sequence 890 BP; 283 A; 179 C; 215 G; 213 T; 0 U; 0 Other;

Query Match 83.8%; Score 744; DB 2; Length 890;
Best Local Similarity 89.9%; Pred. No. 2.5e-138;
Matches 798; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 1 AGCAAAAGCAGGCTGACAAAACATTAATGGATTCCAACTCTGTCTCAAGCTTTAGGTAG 60
DB 1 AGCAAAAGCAGGCTGACAAAACATTAATGGATTCCAACTCTGTCTCAAGCTTTAGGTAG 60
QY 61 ACTGTTTCTTTGGCATGTCGCAAAACGATTTGCGAGACCAAGAACTGGGTGATGCCCAT 120
DB 61 ATTGCTTTCTTTGGCATGTCGCAAAACGATTTGCGAGACCAAGAACTAGGTGATGCCCAT 120
QY 121 TCCTTCACCGGCTTCGCGAGAGACAGAACTCCCTAAAAGGAAGAGGTAGCACTCTTGGTC 180
DB 121 TCCTTCACCGGCTTCGCGAGAGACAGAACTCCCTAAAAGGAAGAGGTAGCACTCTTGGTC 180
QY 181 TGCACATCCGAACAGCCACTCTGTCAGGAAACAGATAGTGGAGCAGATTTCTGGAGAGG 240
DB 181 TGCACATCCGAACAGCCACTCTGTCAGGAAACAGATAGTGGAGCAGATTTCTGGAGAGG 240
QY 241 ATTCAGATGAGGCACTTAAATGACCACTTGCCTCTGTTCTTCCGCTTACGCTACTTAATG 300
DB 241 ATTCAGATGAGGCACTTAAATGACCACTTGCCTCTGTTCTTCCGCTTACGCTACTTAATG 300
QY 301 ACATGACTCTTATGATGATGTCAGAGACTGTCAGGAGCTGGTTCATCTCATGCCCAAGCAAGTAA 360
DB 301 ACATGACTCTTATGATGATGTCAGAGACTGTCAGGAGCTGGTTCATCTCATGCCCAAGCAAGTAA 360
QY 361 CAGGCTCCCTATGATTAAGATGCAACGAGCATCATGATGAAGAACTCATCTACTTAAAG 420
DB 361 CAGGCTCCCTATGATTAAGATGCAACGAGCATCATGATGAAGAACTCATCTACTTAAAG 420
QY 421 CAAACTTTAGTGTGATTTTCGAAAGGCTTCGAGCACTTACTACTTTAGAGCCCTTCCACCG 480
DB 421 CAAACTTTAGTGTGATTTTCGAAAGGCTTCGAGCACTTACTACTTTAGAGCCCTTCCACCG 480
QY 481 AAGAGGAGCAGTCGTTGGCGAAATTTTCCACCTTGGGACTCTTAATGCTTAAGGCTTCCACCG 540
DB 481 AAGAGGAGCAGTCGTTGGCGAAATTTTCCACCTTGGGACTCTTAATGCTTAAGGCTTCCACCG 540
QY 541 AGGATGTCAAAATGCAATTTGGGGTCTCTCATTCGAGAGCTTAAATGGAATGAATACCG 600
DB 541 AGGATGTCAAAATGCAATTTGGGGTCTCTCATTCGAGAGCTTAAATGGAATGAATACCG 600
QY 601 TTAGAAATCTCTGAAACTCTACAGAGATTCGCTTGGAGAAAGCAGTATGAGATGGGAGAC 660
DB 601 TTAGAAATCTCTGAAACTCTACAGAGATTCGCTTGGAGAAAGCAGTATGAGATGGGAGAC 660
QY 661 CTTTCATTCCTCCAAAGCAGAAACGAAATATGCGAGAGAACTTGAAGCTTGAATTTGAA 720
DB 661 CTTTCATTCCTCCAAAGCAGAAACGAAATATGCGAGAGAACTTGAAGCTTGAATTTGAA 720
QY 721 GAAATGAATGCTTTGATTTGAAGAGTGAAGACATTAATGGAATGAATTAATGTTT 780
DB 721 GAAATGAATGCTTTGATTTGAAGAGTGAAGACATTAATGGAATGAATTAATGTTT 780
QY 781 GAAATGAATGCTTTGATTTGAAGAGTGAAGACATTAATGGAATGAATTAATGTTT 840
DB 781 GAAATGAATGCTTTGATTTGAAGAGTGAAGACATTAATGGAATGAATTAATGTTT 840
QY 841 ACTTCTCTGTTTCAGCTTATTTAATGATAAAAAACACCCCTTGTCTTCTA 888
DB 841 ACTTCTCTGTTTCAGCTTATTTAATGATAAAAAACACCCCTTGTCTTCTA 888

244 CAGATGAGGACCTTAATAAGACCAATGCTCTGCTTCTGCTTCAAGCTTACTTAACCTGACA 303
 DB CCGATGAGGACCTTAATAAGACCAATGCTCTGCTTCTGCTTCAAGCTTACTTAACCTGACA 748
 304 TGAATCTTGATGATGCTCAAGAGACTGGTTCATGCTCATGCCCAAGCAGAGAAAGTAACAG 363
 DB TGAATCTTGATGATGCTCAAGAGACTGGTTCATGCTCATGCCCAAGCAGAGAAAGTAACAG 688
 364 GCTCCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 423
 DB GCTCCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 628
 424 ACTTTAGTGTGATTTGCAAGAGCTGGAGACATATATATCTTATGAGCTTCAACCGAG 483
 DB ACTTTAGTGTGATTTGCAAGAGCTGGAGACATATATATCTTATGAGCTTCAACCGAG 568
 484 AAGGAGCAGTCTGTTGGCGAAATTTCAATTTGCTTCTTCAGGACATATATGAGG 543
 DB AAGGAGCAGTCTGTTGGCGAAATTTCAATTTGCTTCTTCAGGACATATATGAGG 598
 544 ATGTCATAAAATGCAATTTGGGGTCTCTCATCGGAGGACTTAAATGGAATGATTAACGGTTA 603
 DB ATGTCATAAAATGCAATTTGGGGTCTCTCATCGGAGGACTTAAATGGAATGATTAACGGTTA 648
 604 GAATCTCTGAACTTACAGAGATTCGCTTGGAGAGCAGTCTATGAGATGAGGAGCTT 663
 DB GAATCTCTGAACTTACAGAGATTCGCTTGGAGAGCAGTCTATGAGATGAGGAGCTT 688
 664 CATTTCCCTCCAAAGCAGAAACGAAATGCGAGAGAAACAAATTTGAGCCAGAGTTTGAAGAA 723
 DB CATTTCCCTCCAAAGCAGAAACGAAATGCGAGAGAAACAAATTTGAGCCAGAGTTTGAAGAA 783
 724 ATAGATGCTGATTTGAAGAGTGCAGATAGATTTGAAATACAGAAATAGTTTGAAG 783
 DB ATAGATGCTGATTTGAAGAGTGCAGATAGATTTGAAATACAGAAATAGTTTGAAG 783
 784 CAATATACATTTATCGAGCTTACAGCTTATGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 843
 DB CAATATACATTTATCGAGCTTACAGCTTATGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 843
 844 TTCTCGTTTCAGCTTATTTATGATTAATAAAACACCTTGT 883
 DB TTCTCGTTTCAGCTTATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 883

RESULT 9
 ID AAQ22332 standard; DNA; 890 BP.
 AC AAQ22332;
 XX 14-JUL-1992 (first entry)
 XX RNA (+), (mRNA) from influenza virus A, synthesised from segment 8.
 XX Segments 1-8; Ann Arbor H2N2; A; B; C; transcription; ss.
 XX Influenza A virus.
 XX WO9203454-A.
 XX 05-MAR-1992.
 XX 13-AUG-1991; 91WO-0050742.
 XX 14-AUG-1990; 90US-00567287.
 XX (ISIS-) ISIS PHARM INC.
 XX Cowseit LM, Ecker DJ;
 XX WPI; 1992-096817/12.
 XX

PT New DNA and RNA hybridising to influenza A, B or C - for diagnosis and
 PT treatment of influenza, esp. influenza B.
 XX Disclosure; Fig 5; 64pp; English.
 XX The RNA sequence is derived influenza virus A, Ann Arbor strain H2N2 of
 CC segment 8. The mRNA of this segment encodes the NS1 and NS2 proteins. The
 CC sequence can be used to design oligonucleotide inhibitors against
 CC influenza virus. See also AAQ22289-22331
 XX
 SQ Sequence 890 BP; 292 A; 177 C; 208 G; 0 T; 213 U; 0 Other;
 Query Match 82.2%; Score 729.6; DB 2; Length 890;
 Best Local Similarity 67.2%; Pred. No. 2.8e-194;
 Matches 597; Conservative 192; Mismatches 99; Indels 0; Gaps 0;
 1 AGCAAAAGCAGGCTGACAAACCAATGGAATTCACACTGTGTCAAGCTTACAGTAG 60
 DB 1 AGCAAAAGCAGGCTGACAAACCAATGGAATTCACACTGTGTCAAGCTTACAGTAG 60
 61 ACTGTTTCTTGGCATGTCCGCAACGATTTGAGACCAAGAACTGTGTGATGCCCAT 120
 DB 61 ACTGTTTCTTGGCATGTCCGCAACGATTTGAGACCAAGAACTGTGTGATGCCCAT 120
 61 AUGCUUCCUUGGCAUUGCCGCAACCAAGUUGCAGACCAAGAACTGTGTGATGCCCAT 120
 DB 61 AUGCUUCCUUGGCAUUGCCGCAACCAAGUUGCAGACCAAGAACTGTGTGATGCCCAT 120
 121 TCCTTGACCGCTTCCGCGAGACCAAGAGTCCCTAAAAGGAGAGGTAGCTCTTGTGTC 180
 DB 121 TCCTTGACCGCTTCCGCGAGACCAAGAGTCCCTAAAAGGAGAGGTAGCTCTTGTGTC 180
 121 UCGUUGAUGGCUUGCGGAGACCAAGAGTCCCTAAAAGGAGAGGTAGCTCTTGTGTC 180
 DB 121 UCGUUGAUGGCUUGCGGAGACCAAGAGTCCCTAAAAGGAGAGGTAGCTCTTGTGTC 180
 181 TGGACATCGAAGACCAAGCACTGTGCGAGGAAAGCAGATAGTGGAGCAGATCTTGGAGAGG 240
 DB 181 TGGACATCGAAGACCAAGCACTGTGCGAGGAAAGCAGATAGTGGAGCAGATCTTGGAGAGG 240
 181 UGAACAUCCAGACCAAGCACTGTGCGAGGAAAGCAGATAGTGGAGCAGATCTTGGAGAGG 240
 DB 181 UGAACAUCCAGACCAAGCACTGTGCGAGGAAAGCAGATAGTGGAGCAGATCTTGGAGAGG 240
 241 AATCAGATGAGCAGCTTAAATGACCATTTGCTCTGTTCTTCTTCAAGCTTAACTG 300
 DB 241 AATCAGATGAGCAGCTTAAATGACCATTTGCTCTGTTCTTCTTCAAGCTTAACTG 300
 241 AUCUUGAUGGCAUUAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 300
 DB 241 AUCUUGAUGGCAUUAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 300
 301 ACATGACTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 DB 301 ACATGACTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 301 AUAUGCUUUGGCAUUAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 360
 DB 301 AUAUGCUUUGGCAUUAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 360
 361 CAGCTCCCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 DB 361 CAGCTCCCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 361 CAGGCCCCUUGGCAUUAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 420
 DB 361 CAGGCCCCUUGGCAUUAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 420
 421 CAATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 DB 421 CAATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 421 CGAAUUCAGUGUGAUAUUGGCAUUAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 480
 DB 421 CGAAUUCAGUGUGAUAUUGGCAUUAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 480
 481 AAGAGGAGCAGCTGCTGCGAAATTTTCAAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 540
 DB 481 AAGAGGAGCAGCTGCTGCGAAATTTTCAAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 540
 481 AAGCGGAGCAGCAUUGGUGGCAUUAUUGGCAUUAUUGGCAUUAUUGGCAUUAUUGGCAU 540
 DB 481 AAGCGGAGCAGCAUUGGUGGCAUUAUUGGCAUUAUUGGCAUUAUUGGCAUUAUUGGCAU 540
 541 AGGATGTCAAAAATGCAATTTGGGCTCTCATCGAGCAGCTTAAATGGAATGATTAATACCG 600
 DB 541 AGGATGTCAAAAATGCAATTTGGGCTCTCATCGAGCAGCTTAAATGGAATGATTAATACCG 600
 541 AGGAUUGCAAAAATGCAUUAUUGGUGGCAUUAUUGGUGGCAUUAUUGGUGGCAUUAUUGG 600
 DB 541 AGGAUUGCAAAAATGCAUUAUUGGUGGCAUUAUUGGUGGCAUUAUUGGUGGCAUUAUUGG 600
 601 TTAGAATCTCTGAAATCTTACAGATTCGCTTGGAGAGCAGTCTGAGAGTGGGAGAC 660
 DB 601 TTAGAATCTCTGAAATCTTACAGATTCGCTTGGAGAGCAGTCTGAGAGTGGGAGAC 660
 601 UUCGAGUCUCUAAAATCTTACAGATTCGCTTGGAGAGCAGTCTGAGAGTGGGAGAC 660
 DB 601 UUCGAGUCUCUAAAATCTTACAGATTCGCTTGGAGAGCAGTCTGAGAGTGGGAGAC 660
 661 CTTCAATCCCTCCAAAGCAGAAACGAAAATGAGAGACCAATTTGAGCAGCAAGTTGAA 720
 DB 661 CTTCAATCCCTCCAAAGCAGAAACGAAAATGAGAGACCAATTTGAGCAGCAAGTTGAA 720
 661 CUCCACUCACUCCCAAAUUAAGAAACGAAAATGAGAGACCAATTTGAGCAGCAAGTTGAA 720
 DB 661 CUCCACUCACUCCCAAAUUAAGAAACGAAAATGAGAGACCAATTTGAGCAGCAAGTTGAA 720
 721 GAAATAAGATGCTGTTGATTTGAAGAAGTGCAGATAGATTTGAATAATGAGAAATAGCTTT 780
 DB 721 GAAATAAGATGCTGTTGATTTGAAGAAGTGCAGATAGATTTGAATAATGAGAAATAGCTTT 780
 721 GAAUUAAGAGGUGGUGAUGAAGAGAGAGACCAAAUUGAAGAAUACAGAGAGAGAGAG 780
 DB 721 GAAUUAAGAGGUGGUGAUGAAGAGAGAGACCAAAUUGAAGAAUACAGAGAGAGAGAG 780
 781 GAACAAATAAGATTTATGCAAGCTTTACAACTATTGCTTGAAGTAGACAGAGATGAA 840
 DB 781 GAACAAATAAGATTTATGCAAGCTTTACAACTATTGCTTGAAGTAGACAGAGATGAA 840
 781 GAGCAAAUUAACAUUUAUGCAAGCTTAAUUAUGAAGGAGGAGGAGGAGGAGGAGGAGGAG 840
 DB 781 GAGCAAAUUAACAUUUAUGCAAGCTTAAUUAUGAAGGAGGAGGAGGAGGAGGAGGAGGAG 840
 841 ACTTCTCTGTTTCTGAGCTTATTTAATGATATAAAAAACACCTTGTCTTCTA 888
 DB 841 ACTTCTCTGTTTCTGAGCTTATTTAATGATATAAAAAACACCTTGTCTTCTA 888

XX	02-MAR-2000; 2000EP-00104338.	Db	541	CCAGGACATATCTGTCAGGATGTCAAAATGTCAGTTGGAGTCTCTCATTCGGGGACTTGAA	600
XX	(POLY-) POLYUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.	Qy	585	TGGAATGATATATACGGTTAGAAATCTTGAAATCTCTACAGATTCCTTGGAGACGAGT	644
XX	Ferko B, Egorov A, Voglauer R;	Db	601	TGGAATGATATACACAGTCAGTTCGAGTCTCTGAACTCTACAGAGATTCCTTGGAGACGAGT	660
XX	WPI; 2001-514840/56.	Qy	645	CATGAGATGGGAGACCTTCATTCCTCCAAAGCAGAAACGAAATTCGAGAGACAAATTT	704
XX	Recombinant NS gene of an influenza A virus comprising a functional RNA	Db	661	AATGAGATGGGAGACCTTCCTCACTCACTCAAAACAGAAACGAGAAATTCGCGGAGCAAT	720
XX	binding domain and a gene sequence modification after nucleotide position	Qy	705	GAGCAGAGATGTTTGAGAAATAGATGGTTGATTGAGAGAGTCCGACATAGATTGAAAAA	764
XX	400 of the NS1 gene segment, useful for producing a live attenuated	Db	721	AGTCAGAGATGTTTGAGAAATAGATGGTTGATTGAGAGAGTCCGACATAGATTGAAAAA	780
XX	influenza virus vaccine.	Qy	765	TACAGAAATATAGTTTTCAGCAATTAACATTTATGCAAGCCTTACAACTATTGCTTGAAGT	824
XX	Example 6; Page 21; 40pp; English.	Db	781	ACACAGAGATGTTTTCAGCAATTAACATTTATGCAAGCCTTACAACTATTGCTTGAAGT	840
XX	The specification describes a recombinant nonstructural (NS) gene of an	Qy	825	AGACAGAGATGATAGAACTTTCTCGTTTCAGCTTATTATGATATAAAAAACACCTTGT	884
XX	influenza A virus. The gene comprises a functional RNA binding domain and	Db	841	GGAGCAGAGATGATAGAACTTTCTCGTTTCAGCTTATTATGATATAAAAAACACCTTGT	900
XX	a gene sequence modification after nucleotide position 400 of the NS1	Qy	885	TCTA 888	
XX	gene segment, counted on the basis of influenza A/PR/8/34 virus, where	Db	901	TCTA 904	
XX	the modification base transcription of the remaining portion of the NS1				
XX	gene segment. The recombinant NS gene is used to produce a vaccine, which				
XX	is useful for prophylactic or therapeutic application against a viral				
XX	infection, preferably against influenza or HIV-1 infection. Influenza				
XX	virus transfectants that contain the modified NS gene may have an				
XX	interferon (IFN) inducing phenotype, but may or may not be sensitive				
XX	towards to IFN. The present sequence was used to construct vectors for				
XX	production of modified NS genes of the invention				
XX	Sequence 906 BP; 288 A; 183 C; 221 G; 214 T; 0 U; 0 Other;				
XX	Query Match 79.5%; Score 706.4; DB 4; Length 906;				
XX	Best Local Similarity 88.2%; Pred. No. 9.3e-188;				
XX	Matches 797; Conservative 91; Mismatches 91; Indels 16; Gaps 2;				
Qy	1 AGCAAGACAGGGTGCACAAACATATGATGATTCACACACTGTGTCAAGCTTTCAGGTAG 60				
Db	1 AGCAAGACAGGGTGCACAAACATATGATGATTCACACACTGTGTCAAGCTTTCAGGTAG 60				
Qy	61 ACTGTTTCTTGGCATGTCGCAACAGATTTGCAGACCAAGAACTGGGTGATGCCCAT 120				
Db	61 ATTGCTTCTTGGCATGTCGCAACAGATTTGCAGACCAAGAACTGGGTGATGCCCAT 120				
Qy	121 TCCTTGACGGCTTCCCGAG-----ACCAGAGTCTCTAAAGGAAGAG 165				
Db	121 TCCTTGATCGGCTTCCCGAGTGAATAGTGAATCAGAAATCCCTAAGAGGAAGG 180				
Qy	166 GTAGACATCTTGTCTGGACATCGAAGACGCACTCTGTCAGGAAAGCAGATAGTGGAGC 225				
Db	181 GCAGACCCCTCGGTCTGGACATCGAAGACGCACTCTGTCAGGAAAGCAGATAGTGGAGC 240				
Qy	226 AGATTCTGGAAGAGGAATCAGATGAGGCACTTAAATGACCAATTCCTGTTCTGCTT 285				
Db	241 GGATTCTGGAAGAGGAATCCGATGAGGCACTTAAATGACCAATTCCTGTTCTGCTT 300				
Qy	286 CACGCTACTTAACTGACATGCTCTGATGATGTCAGAGACTGTTTCATGCTCATGTC 345				
Db	301 CGCGTTACTTAACTGACATGCTCTGATGATGTCAGAGACTGTTTCATGCTCATGTC 360				
Qy	346 CCAAGCAGAAAGTAA CAGGCTCCCTATGTTATAGATGACACGACCAATCGA--TAG 404				
Db	361 CCAAGCAGAAAGTGGCAGGCTCTTGTATGATGATGACACGACCAATCATGATTAG 420				
Qy	405 AACATCATCTTAAAGCAAACTTTAGTGTGATTTTGAAGGCTGGAGCACTAATCTA 464				
Db	421 AACATCATCTTAAAGCAAACTTTAGTGTGATTTTGAAGGCTGGAGCACTAATCTA 480				
Qy	465 CTTAGAGCTTTCACCGAAGAGGACAGTCTGTGGCGAAATTTCACTTCCCTCTCT 524				
Db	481 CTAAGGGCTTTCACCGAAGAGGAGCAATTTGTGGCGAAATTTCACTTCCCTCTCT 540				
Qy	525 CCAGAGACATCTAATAGGATGTCAAAAATCAATTTGGGCTCTCATCGAGGACTTAA 584				

Db	541	CCAGGACATATCTGTCAGGATGTCAAAATGTCAGTTGGAGTCTCTCATTCGGGGACTTGAA	600
Qy	585	TGGAATGATATATACGGTTAGAAATCTTGAAATCTCTACAGATTCCTTGGAGACGAGT	644
Db	601	TGGAATGATATACACAGTCAGTTCGAGTCTCTGAACTCTACAGAGATTCCTTGGAGACGAGT	660
Qy	645	CATGAGATGGGAGACCTTCATTCCTCCAAAGCAGAAACGAAATTCGAGAGACAAATTT	704
Db	661	AATGAGATGGGAGACCTTCCTCACTCACTCAAAACAGAAACGAGAAATTCGCGGAGCAAT	720
Qy	705	GAGCAGAGATGTTTGAGAAATAGATGGTTGATTGAGAGAGTCCGACATAGATTGAAAAA	764
Db	721	AGTCAGAGATGTTTGAGAAATAGATGGTTGATTGAGAGAGTCCGACATAGATTGAAAAA	780
Qy	765	TACAGAAATATAGTTTTCAGCAATTAACATTTATGCAAGCCTTACAACTATTGCTTGAAGT	824
Db	781	ACACAGAGATGTTTTCAGCAATTAACATTTATGCAAGCCTTACAACTATTGCTTGAAGT	840
Qy	825	AGACAGAGATGATAGAACTTTCTCGTTTCAGCTTATTATGATATAAAAAACACCTTGT	884
Db	841	GGAGCAGAGATGATAGAACTTTCTCGTTTCAGCTTATTATGATATAAAAAACACCTTGT	900
Qy	885	TCTA 888	
Db	901	TCTA 904	
XX	RESULT 12		
XX	ADY62118		
XX	ID ADY62118 standard; DNA; 824 BP.		
XX	AC ADY62118;		
XX	DT 19-MAY-2005 (first entry)		
XX	DE Influenza A virus strain A/England/1/53v-a mutant NS1 gene for vaccine.		
XX	DE protein engineering; immune stimulation; immunostimulant; vaccine;		
XX	KW Influenza virus infection; mutant; gene; ds.		
XX	OS Influenza A virus; strain A/England/1/53v-a.		
XX	Key Location/Qualifiers		
XX	CDS 6..698		
XX	FT /*tag= a		
XX	FT /product= "mutated influenza A virus NS1 protein"		
XX	US2005054846-A1.		
XX	10-MAR-2005.		
XX	04-SEP-2003; 2003US-00654737.		
XX	04-SEP-2003; 2003US-00654737.		
XX	(WEBB/) WEBSTER R G.		
XX	(WEBB/) WEBBY R J.		
XX	(OZAK/) OZAKI H.		
XX	Webster RG, Webby RJ, Ozaki H;		
XX	WPI; 2005-213104/22.		
XX	P-PSDB; ADY62121.		
XX	Producing a reassortant influenza virus that gives a high titer in Vero		
XX	cells (certified for use in vaccine-production), comprises replacing the		
XX	NS gene of the A/PuertoRico/3/24 master strain with the NS gene of the		
XX	A/England/1/53 strain.		
XX	Claim 8; SEQ ID NO 2; 16pp; English.		
XX	The invention relates to a method of producing a high titer reassortant		
XX	influenza virus by transfecting host cells with expression plasmids		
CC			

CC containing the PB2, PB1, PA, NP, and M genes from the A/PuertoRico/8/34
 CC influenza strain, the NS gene from the A/England/1/53 influenza strain,
 CC and the HA and NA genes from an influenza virus of interest other than
 CC A/England/1/53, to obtain a high titer reassortant influenza virus. The
 CC method is useful for producing a high titer reassortant influenza virus.
 CC The high titer reassortant influenza viruses are useful for producing
 CC vaccine compositions. The vaccines are useful for treating or preventing
 CC influenza viral infections. Genetic engineering techniques allow the
 CC rapid production of custom made attenuated virus vaccines, but vaccine
 CC use is limited by the need to use vaccine approved cell lines. The master
 CC strain A/PuertoRico/8/34 which is the most widely used in producing
 CC recombinant viruses for vaccine use produces a high titer in MDCK cells,
 CC which are not certified for use in production of human vaccines, but not
 CC in vero cells, which are certified for this use. The applicants have
 CC discovered that replacing the NS gene of the A/PuertoRico/3/24 master
 CC strain with the NS gene of the A/England/1/53 strain gives reassortant
 CC virus that produces a high titer in vero cells. This sequence corresponds
 CC to the coding sequence for the NS1 protein from the A/England/1/53v-a
 CC influenza strain. This strain encodes the protein with the amino acid
 CC changes Q21R/T58I/V60A/N127S/V174I/D189N/delta231-238.
 CC
 XX Sequence 824 BP; 263 A; 167 C; 203 G; 191 T; 0 U; 0 Other;

Query Match 78.0%; Score 692.8; DB 14; Length 824;
 Best Local Similarity 90.0%; Pred. No. 5.9e-184;
 Matches 742; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
 OY 22 ACATATGATTCGACACACTGTGTCAAGCTTTCAGGTAGACTGTTTCTTTGGCATGTC 81
 DB 1 ACATATGATTCGACACACTGTGTCAAGCTTTCAGGTAGACTGTTTCTTTGGCATGTC 60
 OY 82 GCAACAGATTTCGAGACCAAGAACTGGGTGATGCCCATTCCTTTGACCGGCTTCGCCGAG 141
 DB 61 GCAACAGATTTCGAGACCAAGAACTAGGTGATGCCCATTCCTTTGATCGGCTTCGCCGAG 120
 OY 142 ACCAGAAATCCCTAAAGAGAGAGTGTGACATCTTGGTCTGGACATCGAAACAGCCACTC 201
 DB 121 ATCAGAAATCCCTAAAGAGAGAGTGTGACATCTTGGTCTGGACATCGAAACAGCCACTC 180
 OY 202 GTCCAGAGAGAGAGTGTGAGCAGATTCGAGAGAGATCAGATGAGCAGCTTAAATA 261
 DB 181 GTCTGAGAGAGAGATGTGAGCGGATTCGAGAGAGATCCGATGAGCAGCTTAAATA 240
 OY 262 TGACATGTCCTTGTCTGCTTCAAGCTTAACTGACATGATCTTGTAGATGATGT 321
 DB 241 TGACATGTCCTTGTCTGCTTCAAGCTTAACTGACATGATCTTGTAGATGATGT 300
 OY 322 CAAGAGACTGGTTCATGCTCATGCCCAAGCAGAAAGTAACAGGCTCCCTATGTATAAGAA 381
 DB 301 CAAGAGACTGGTTCATGCTCATGCCCAAGCAGAAAGTGGCAGGCTCTTGTATCAAGAA 360
 OY 382 TGACACAGGCAATCATGTATAAGAAATCATATCTTAAAGCAAACTTTTACTGTGATTTTCG 441
 DB 361 TGACACAGGCAATCATGTATAAGAAATCATATCTTAAAGCAAACTTTTACTGTGATTTTG 420
 OY 442 AAAGCTTGAGAGACATACTACTTACTAGGCTTCAAGAGAGAGAGCAGTGTGGCG 501
 DB 421 ACCGCTTGAGAGACATACTACTTACTAGGCTTCAAGAGAGAGAGCAGTGTGGCG 480
 OY 502 AAATTTACCAATTCCTTCTTCCAGGACATCATTAATGAGGATGTCAAAATGCAATTG 561
 DB 481 AAATTTACCAATTCCTTCTTCCAGGACATCATTAATGAGGATGTCAAAATGCAATTG 540
 OY 562 GGGTCTCTCATCGGAGGACTTAAATGGAATGATAATAACAGTTCAGTCTCTAAATCTCTAC 621
 DB 541 GGGTCTCTCATCGGAGGACTTAAATGGAATGATAATAACAGTTCAGTCTCTAAATCTCTAC 600
 OY 622 AGAGATTCCTTGGAGAGAGTGTGAGATGAGAGAGCTTCATTCCTTCCCAAGAGAGA 681
 DB 601 AGAGATTCCTTGGAGAGAGTGTGAGATGAGAGAGCTTCATTCCTTCCCAAGAGAGA 660
 OY 682 AATGAAATGAGAGAGAGTGTGAGAGAGTGTGAGAGATGAGATGAGTGTGATGAA 741

DB 661 AACGGAAATGCGGAGAACAAATTAGTGTAGAGAAATTAAGATGTTGATTGAA 720
 OY 742 GAAGTGCAGATAGATTCGAAATATACAGAAATAGTTTGAACAATAACATTTATGCA 801
 DB 721 GAAGTGCAGACAGACTCAAGATTAACAGAGATAGTTTGAACAATAACATTTATGCA 780
 OY 802 GCCTTACACTATTCCTTGAAGTAGACACAGAGATGAAGACTTT 845
 DB 781 GCCTTACACTATTCCTTGAAGTAGACACAGAGATGAAGACTTT 824

RESULT 13

AAT37435

ID AAT37435 standard; DNA; 693 BP.

XX AAT37435;

XX AC AAT37435;

XX DT 16-OCT-2003 (revised)

XX DT 09-APR-1997 (first entry)

XX DE Non-structural protein NS1 of influenza A virus.

XX KW Non-structural protein; NS1; influenza virus; respiratory tract;
 XX KW diagnosis; anti-NS1 antibody; primer; PCR; detection; amplify; ss.
 XX OS Influenza virus; A/equine 1/Suffolk 89.

XX PN BP726316-A2.

XX PD 14-AUG-1996.

XX PF 31-JAN-1996; 96BP-00300681.

XX PR 09-FEB-1995; 95GB-00002489.

XX PA (ANIM-) ANIMAL HEALTH TRUST.

XX PI Binns M, Birch-Machin I;

XX DR WPI: 1996-364394/37.

XX DR P-PSDB; AAW03522.

XX PT Recombinant equine influenza virus NS1 protein - useful for diagnosis of
 equine influenza A.
 XX PS Claim 1; Fig 1A; 20pp; English.

XX CC This sequence encodes non-structural protein NS1 of influenza virus
 A/equine 2/Suffolk 89. The NS1 protein is useful for diagnosis of equine
 CC influenza A infections by detection of anti-NS1 antibodies. The NS1
 CC coding sequence was isolated using the primer sequences given in AAT37436
 CC -40. (Updated on 16-OCT-2003 to standardise OS field)

XX SQ Sequence 693 BP; 215 A; 146 C; 166 G; 166 T; 0 U; 0 Other;

Query Match 77.1%; Score 685; DB 2; Length 693;

Best Local Similarity 99.3%; Pred. No. 8.5e-182;

Matches 688; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 27 ATGGATTCACCAACTGTGTCAAGCTTTCAGGTAGACTGTTTCTTTGGCATGTCGCAAA 86

DB 1 ATGGATTCACCAACTGTGTCAAGCTTTCAGGTAGACTGTTTCTTTGGCATGTCGCAAA 60

OY 87 CGATTTTCAGACCAAGAACTGGGTGATGCCCATTCCTTGACCGGCTTGGCCGAGACAG 146

DB 61 CGATTTTCAGACCAAGAACTGGGTGATGCCCATTCCTTGACCGGCTTGGCCGAGACAG 120

OY 147 AAGTCCCTTAAAGAGAGGTAGCAGCTTCTTGTCTGAGACATCGAAACGCCACTCGTCA 206

DB 121 AAGTCCCTTAAAGAGAGGTAGCAGCTTCTTGTCTGAGACATCGAAACGCCACTCGTCA 180

OY 207 GGAAAGCAGATAGTGGAGCAGATTCTTGGAGAGAGTTCAGATGAGGCACTTAAATGACC 266

Db 181 GGAAGCAGATAGTGGAGCAGATTTCTGGAAGAGGATCAGATGAGGCATTTAAATGACC 240
 Qy 267 ATGCTCTCTGTTCTGCTTCAAGCTTACTTAACTGATGATGATGATGATGATGATGATGAT 326
 Db 241 ATTGCTCTGTTCTGCTTCAAGCTTACTTAACTGATGATGATGATGATGATGATGATGAT 300
 Qy 327 GACTGGTCTATGCTATGCTTCAAGCTTACTTAACTGATGATGATGATGATGATGATGATGAT 386
 Db 301 GACTGGTCTATGCTTCAAGCTTACTTAACTGATGATGATGATGATGATGATGATGATGAT 360
 Qy 387 CAGGCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 446
 Db 361 CAGGCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 Qy 447 CTGGAGACACTAATCTACTTACGATGATGATGATGATGATGATGATGATGATGATGATGAT 506
 Db 421 CTGGAGACACTAATCTACTTACGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 Qy 507 TCACCAATGCTTCTCTTCCAGGACATCTAATGAGGATGATGATGATGATGATGATGATGATGAT 566
 Db 481 TCACCAATGCTTCTCTTCCAGGACATCTAATGAGGATGATGATGATGATGATGATGATGATGAT 540
 Qy 567 CTCATCGAGGACTTAAATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 626
 Db 541 CTCATCGAGGACTTAAATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 Qy 627 TTCGCTTGGAGAGCAGTCTATGAGATGAGGAGACCTTCAATTCCTCCAAAGCAGAAACGA 686
 Db 601 TTCGCTTGGAGAGCAGTCTATGAGATGAGGAGACCTTCAATTCCTCCAAAGCAGAAACGA 660
 Qy 687 AATATGAGAGAACAAATGAGCCAGAGATTTGA 719
 Db 661 AATATGAGAGAACAAATGAGTCAAGATTTGA 693

RESULT 14
 ID ADY62117
 AC AC
 XX ADY62117;
 XX 19-MAY-2005 (first entry)
 XX Influenza A virus strain A/England/1/53 wild type NS1 gene for vaccine.
 XX protein engineering; immune stimulation; immunostimulant; vaccine;
 XX Influenza virus infection; gene; ds.
 XX Influenza A virus; strain A/England/1/53.
 XX Key Location/Qualifiers
 CDS 6..719
 FT /*tag= a
 FT /product= "influenza A virus NS1 protein"
 FT /note= "no stop codon given"
 XX US2005054846-A1.
 XX 10-MAR-2005.
 XX 04-SEP-2003; 2003US-00654737.
 XX 04-SEP-2003; 2003US-00654737.
 XX (WEBS/) WEBSTER R G.
 XX (WEBB/) WEBBY R J.
 XX (OZAK/) OZAKI H.
 XX Webster RQ, Webby RJ, Ozaki H;
 XX WPI; 2005-213104/22.
 DR P-PSDB; ADY62119.
 XX

PT Producing a reassortant influenza virus that gives a high titer in Vero
 PT cells (certified for use in vaccine-production), comprises replacing the
 PT NS gene of the A/PuertoRico/3/24 master strain with the NS gene of the
 PT A/England/1/53 strain.
 XX
 PS Claim 7; SEQ ID NO 1; 16pp; English.
 XX
 CC The invention relates to a method of producing a high titer reassortant
 CC influenza virus by transfecting host cells with expression plasmids
 CC containing the PB2, PB1, PA, NP, and M genes from the A/PuertoRico/8/34
 CC influenza strain, the NS gene from the A/England/1/53 influenza strain,
 CC and the HA and NA genes from an influenza virus of interest other than
 CC A/England/1/53, to obtain a high titer reassortant influenza virus. The
 CC method is useful for producing a high titer reassortant influenza virus.
 CC The high titer reassortant influenza viruses are useful for producing
 CC vaccine compositions. The vaccines are useful for treating or preventing
 CC influenza viral infections. Genetic engineering techniques allow the
 CC rapid production of custom made attenuated virus vaccines, but vaccine
 CC use is limited by the need to use vaccine approved cell lines. The master
 CC strain A/PuertoRico/8/34 which is the most widely used in MDCK cells,
 CC recombinant viruses for vaccine use produces a high titer in MDCK cells,
 CC which are not certified for use in production of human vaccines, but not
 CC in Vero cells, which are certified for this use. The applicants have
 CC discovered that replacing the NS gene of the A/PuertoRico/3/24 master
 CC strain with the NS gene of the A/England/1/53 strain gives reassortant
 CC virus that produces a high titer in Vero cells. This sequence corresponds
 CC to the coding sequence for the NS1 protein from the A/England/1/53
 CC influenza strain.
 XX
 SQ Sequence 824 BP; 267 A; 167 C; 201 G; 189 T; 0 U; 0 Other;

Query Match 77.1%; Score 684.8; DB 14; Length 824;
 Best Local Similarity 89.4%; Pred. No. 16-181;
 Matches 737; Conservative 0; Mismatches 87; Indels 0; Gaps 0;
 Qy 22 ACATATGATGTTCCAAACACCTGTCAGCTTTTCAGTGTAGTCTTTTTCATGTCATGTC 81
 Db 1 ACATATGATGTTCCAAACACCTGTCAGCTTTTCAGTGTAGTCTTTTTCATGTCATGTC 60
 Qy 82 GCAAAACGATTTGACAGCAGCAAGCTGGGTGATGCCCCCATCTCTGACGGCTTCGCCGAG 141
 Db 61 GCAAAACGATTTGACAGCAGCAAGCTGGGTGATGCCCCCATCTCTGATGCGCTTCGCCGAG 120
 Qy 142 ACCAGAGTCCCTTAAAGAGAGAGTGTAGTCACTCTGTTGTCGACATCGAAACAGGCACATC 201
 Db 121 ATCAGAGTCCCTTAAAGAGAGAGTGTAGTCACTCTGTTGTCGACATCGAAACAGGCACATC 180
 Qy 202 GTGACGAGAAAGCAGATAGTGGAGCAGATTTCTGGAAGAGGATCAGATGAGSCACTTAAAA 261
 Db 181 GTGTTGAAAGCAGATAGTGGAGCAGATTTCTGGAAGAGGATCAGATGAGSCACTTAAAA 240
 Qy 262 TGACCATGCTCTGTTCTCTTCTTCACTGCTTCACTTAACTGATGATGATGATGATGATGATG 321
 Db 241 TGACCATGCTCTGTTCTCTTCTTCACTGCTTCACTTAACTGATGATGATGATGATGATGATG 300
 Qy 322 CAAGAGACTGGTTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTT 381
 Db 301 CAAGAGACTGGTTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTT 360
 Qy 382 TGGACACGAGCAATCATGATAGAAACATCATCATCTTAAAGCAACTTTAGTGTGATTTTCG 441
 Db 361 TGGACACGAGCAATCATGATAGAAACATCATCATCTTAAAGCAACTTTAGTGTGATTTTCG 420
 Qy 442 AAAGGCTGAGACACTAATACTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTT 501
 Db 421 ACCGGCTGAGACACTAATACTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTT 480
 Qy 502 AAATTTTCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 561
 Db 481 AAATTTTCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 540
 Qy 562 GGTCTCTCATCGAGGACTTAAATGGAATGATTAATGATTAATGATTAATGATTAATGATTAAT 621

Db 541 GGCTCCTCATCGGAGCTTGAATGAATGATTAACACAGTTCGAGTCTCTAAACTCTAC 600
 Qy 622 AGAGATTTCGCTTGAGAGAGCAGTCAATGAGATGGAGACCTTCATTCCCTCCAAAGCAGA 681
 Db 601 AGAGATTTCGCTTGAGAGAGCAGTCAATGAGATGGAGACCTTCACCTCACTCCAAACAGA 660
 Qy 682 AACGAAATATGAGAGAGCAATTTGAGCCAGAGTTTCAAGAAATAGATGTTGATTGAA 741
 Db 661 AACGAAATATGAGAGAGCAATTTGAGCCAGAGTTTCAAGAAATAGATGTTGATTGAA 720
 Qy 742 GAAGTGCACATACATTTGAATATACAGAAATAGTTTGAACAAATACATTTATCGAA 801
 Db 721 GAAGTGCACATACATTTGAATATACAGAAATAGTTTGAACAAATACATTTATCGAA 780
 Qy 802 GCCTTACAACTATTCTTGAAGTGAACAGAGATAGAACTTT 845
 Db 781 GCCTTACAACTATTCTTGAAGTGAACAGAGATAGAACTTT 824

RESULT 15

AAD15680
 ID AAD15680 standard; DNA; 468 BP.

AC AAD15680;

DT 15-NOV-2001 (first entry)

DE Equine influenza virus H3N8 neiwt4NS468 DNA.

KW Equine influenza virus; ei; cold adaptation; temperature sensitivity;
 KW vaccine; neiwt4NS468 DNA; Peiwt4NS97 protein; ds.

OS Equine influenza virus H3N8.

PH Key Location/Qualifiers

FT misc_feature 1..293

FT /tag= b

FT /note= "This region is specifically claimed as SEQ ID NO:
 FT 38 in claim 2 of the specification"

FT CDS 3..296

FT /tag= a "Peiwt4NS97 protein /note "CDS does not include
 FT /products start codon"
 FT /partial

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CC protecting animals from diseases caused by influenza viruses. They are
 CC also used as vaccines. The present sequence is equine influenza (ei)
 CC virus H3N8 neiwt4 (wild type) NS468 DNA encoding Peiwt4NS97 protein
 XX
 SQ Sequence 468 BP; 168 A; 80 C; 98 G; 122 T; 0 U; 0 Other;

Query Match 52.2%; Score 463.4; DB 4; Length 468;

Best Local Similarity 99.8%; Pred. No. 1.3e-119;

Matches 464; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 424 ACTTATGCTGATTTTCGAAAGCTGGAGACACTAATACTACTACTAGAGCTTCACCGAAG 483

Db 1 ACTTATGCTGATTTTCGAAAGCTGGAGACACTAATACTACTACTAGAGCTTCACCGAAG 60

Qy 484 AAGGACAGTCTGCTGGCGAAATTTCCACATTCGCTTCTCTCCAGACATACATAGAGG 543

Db 61 AAGGACAGTCTGCTGGCGAAATTTCCACATTCGCTTCTCTCCAGACATACATAGAGG 120

Qy 544 ATGTCAAAAATGCAATTTGGGGTCTCATTCGAGAGCTTTAAATGAATGATAATACGGTTA 603

Db 121 ATGTCAAAAATGCAATTTGGGGTCTCATTCGAGAGCTTTAAATGAATGATAATACGGTTA 180

Qy 604 GAATCTCTGAAACTCTACAGAGATTCGCTTGGAGAGCAGTCAATGAGAAATGGAGACCTT 663

Db 181 GAATCTCTGAAACTCTACAGAGATTCGCTTGGAGAGCAGTCAATGAGAAATGGAGACCTT 240

Qy 664 CATTCCCTCCAAAGCAGAAAACGAAAATGGAGAGAACAAATTTGAGCCAGAGTTTGAAGAA 723

Db 241 CATTCCCTCCAAAGCAGAAAACGAAAATGGAGAGAACAAATTTGAGCCAGAGTTTGAAGAA 300

Qy 724 ATAAGATGCTTGAATGAAAGTGGCAGATAGATTGAAAATAACAGAAAATAGTTTTCGAA 783

Db 301 ATAAGATGCTTGAATGAAAGTGGCAGATAGATTGAAAATAACAGAAAATAGTTTTCGAA 360

Qy 784 CAAATAACATTTATGCAAGCTTACAACTATTGCTTGAAGTAGAACAAGAGATAAGAACT 843

Db 361 CAAATAACATTTATGCAAGCTTACAACTATTGCTTGAAGTAGAACAAGAGATAAGAACT 420

Qy 844 TTCTCGTTTTCAGCTTATTTAATGATAAATAACACACCTTGTTTCTA 888

Db 421 TTCTCGTTTTCAGCTTATTTAATGATAAATAACACACCTTGTTTCTA 465

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Job time : 561.673 secs

Claim 2; Page 74-75; 172pp; English.

The patent discloses cold-adapted equine influenza viruses and
 reassortant influenza A viruses comprising at least one genome segment of
 such an equine influenza virus, wherein the equine influenza virus genome
 segment confers at least one identifying phenotype of the cold-adapted
 equine influenza virus, such as cold adaptation, temperature sensitivity,
 dominant interference or attenuation. The viruses are useful for

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OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 00:06:39 ; Search time 4487.83 Seconds
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Searched: 41078325 seqs, 23393541228 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: gb_est2.*
- 3: gb_est3.*
- 4: gb_est4.*
- 5: gb_est5.*
- 6: gb_est6.*
- 7: gb_est7.*
- 8: gb_est8.*
- 9: gb_est9.*
- 10: gb_est10.*
- 11: gb_est11.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59.4	6.7	1101	CNS0039G	AL063921 Drosophil
2	55.2	6.2	1101	CNS0006J	AL062049 Drosophil
3	54.8	6.2	899	CNS03X3Y	AL264535 Tetradon
4	48.6	5.5	929	CNS07BEP	AL437783 T7 end of
5	47.2	5.3	1164	CL035484	CL035484 CH216-39N
6	47.2	5.3	1227	CK210809	CK210809 FGAS02263
7	47	5.3	1101	CNS0039R	AL063932 Drosophil
8	46.4	5.2	576	CE229067	CE229067 tigr-gss-
9	46.4	5.2	1268	AG311044	AG311044 Mus muscu
10	46.2	5.2	675	BH988095	BH988095 oeJ25a02.
11	46.2	5.2	759	CNS060XV	AL411257 T7 end of
12	46.2	5.2	857	9 AZ688092	AZ688092 ENTKB44TR
13	46.2	5.2	1316	AG304883	AG304883 Mus muscu
14	46.2	5.2	2565	AK020016	AK020016 Mus muscu
15	45.6	5.1	1514	AG311217	AG311217 Mus muscu
16	45.4	5.1	521	9 BH71630	BH71630 BOGR93TR
17	45.4	5.1	701	9 BH711431	BH711431 BOMF59TF
18	45.2	5.1	408	10 CNS009R3	AL054432 Drosophil
19	45.2	5.1	645	3 BM167957	BM167957 EST570520
20	45.2	5.1	947	10 CWS951010	CWS951010 TcB36.2_E
21	45.2	5.1	1213	10 AG277918	AG277918 Mus muscu
22	45	5.1	718	9 BZ510433	BZ510433 BOMRC82TF

ALIGNMENTS

RESULT 1
CNS0039G/c

LOCUS 1101 bp DNA linear GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL063921
VERSION AL063921.1 GI:4941778
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
AUTHORS
TITLE
JOURNAL

Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org>. The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oosagawa and Aaron Mammeter in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
source

1. .1101
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ORIGIN

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C 25	44.6	5.0	857	10	CNS01831
C 26	44.6	5.0	2017	4	AK090268
C 27	44.4	5.0	687	9	BH723944
C 28	44.4	5.0	760	9	BZ461276
C 29	44.4	5.0	1116	10	CL116360
C 30	44.4	5.0	1201	10	CNS018FX
C 31	44.2	5.0	823	10	CWS95861
C 32	44.2	5.0	859	10	CZ958571
C 33	44.2	5.0	899	10	CWS947334
C 34	44	5.0	509	3	BM952076
C 35	44	5.0	665	2	BG854775
C 36	44	5.0	666	9	CC964338
C 37	44	5.0	704	9	BH941436
C 38	44	5.0	705	9	BH485727
C 39	43.8	4.9	618	9	BH657329
C 40	43.8	4.9	631	10	CNS02NKC
C 41	43.8	4.9	964	11	CNS07B8R
C 42	43.6	4.9	375	10	CE364194
C 43	43.6	4.9	1129	10	AG305138
C 44	43.6	4.9	1203	10	AG377060
C 45	43.4	4.9	443	3	BM170766

AZ138945 SP_0179_B
AG278227 Mus muscu
AL108923 Drosophil
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BH723944 BOMEZ22TF
BZ461276 BOMDR60TF
CL116360 ISR1-65D2
AL106895 Drosophil
CWS95861 TcB40.1.D
CZ958571 187959 To
CWS947334 TcB30.3.D
BM952076 rc55a04.Y
BG854775 1024040G1
CC964338 BOICB08TF
BH941436 od940h01.
BH485727 BOGLF32TF
BH657329 BOMFB36TR
AL205509 Tetradon
AL441457 T7 end of
CE364194 tigr-gss-
AG305138 Mus muscu
AG377060 Mus muscu
BM170766 EST573289

RESULT 2	CNS0006J	linear	GSS 03-JUN-1999
JOCUS	NS0006J	DNA	
DEFINITION	Drosophila melanogaster genome survey sequence TET3 end of BAC # BAC01M22 of RPCL-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.		
ACCESSION	AL062043.1		
VERSION	AL062043.1		GI:4938511
KEYWORDS	GSS: drosophila melanogaster (fruit fly)		
SOURCE	Drosophila melanogaster		
ORGANISM	Drosophila melanogaster		
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		
AUTHORS	1. (bases 1 to 1101)		
TITLE	Genoscope.		
JOURNAL	Direct Submission		
COMMENT	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 1191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://flyw.flyw.flyw.org The BDGP Drosophila melanogaster BAC library was prepared by Kasutogo Oosagawa and Aaron Mammeter in Peter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCL-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y; cn, bw, sp, the same strain used for the BDGP's		

RESULT 3	
LOCUS	CNS03X3Y/c
DEFINITION	899 bp DNA linear GSS 01-SEP-2000 Tetraodon nigroviridis genome survey sequence pUC-Ori end of clone 065B07 of library G from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION	CNS03X3Y
VERSION	AL264535.1 GI:7986236
KEYWORDS	GSS: genome survey sequence.
SOURCE	Tetraodon nigroviridis
ORGANISM	Tetraodon nigroviridis
REFERENCE	1 Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Winkler,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J. Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000) 10835645
REFERENCE	2 Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000) 10899143
REFERENCE	3 Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Winkler,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J. Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000) 10835645
REFERENCE	4 Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Winkler,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000) 10899143

ORGANISM *Xenopus tropicalis*
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Xenopus; Silurana.
AUTHORS Krenitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T., Madis, E., and Wilson, R.
TITLE A physical map of the *Xenopus tropicalis* genome
JOURNAL Unpublished (2003)
COMMENT Contact: Richard K Wilson
 Genome Sequencing Center
 Washington University School of Medicine
 Email: submit88@wustl.edu
 Insert Length: 75000 Std Error: 0.00
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 High quality sequence start: 18
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 Best Local Similarity 52.0%; Pred. No. 0.18; 98; Indels 0; Gaps 0;
 Matches 106; Conservative 0; Mismatches 0;

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 Best Local Similarity 47.6%; Pred. No. 0.19; Indels 0; Gaps 0;
 Matches 100; Conservative 0; Mismatches 110;

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 Db 558 AAGAATATAGGTATATATTATGAGATGATATACGAATAGAGTAGTATATAATAA 499
 |||||
 QY 735 GATTGAGAGGTGCGACATAGATGGAATATAGAAATAGTTTGGACAAATACATT 794
 |||||
 Db 498 TAGTCAAGAGAAATTAATGTTGGAAATATAGAAATATTAATTAATTTT 439
 |||||
 QY 795 TATCAAGCCCTTACACATTTGTTGAGTACAGACAGATAGACTTCTCGTTCA 854
 |||||
 Db 438 TAAAAAGCGATTAGATATTGTTGGGGGGGAGAGAAATTAATTAATTTAGTATGC 379
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 QY 855 GCTTATTTATGATAAAAACACC 878
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 Db 378 AAGGATATATGATAAATACAC 355

RESULT 6
 CK210809 1227 bp mRNA linear EST 08-DEC-2003
 LOCUS FGAS022636 Triticum aestivum FGAS: Library 5 GATE 7 Triticum
 DEFINITION aestivum cDNA, mRNA sequence.
 CK210809 1 GI:39573199
 VERSION EST.
 KEYWORDS Triticum aestivum (bread wheat)
 SOURCE Triticum aestivum
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.
 1 (bases 1 to 1227)
 Allard, F., Crosby, W.L., Danyluk, J., Rudes, F., Frick, M., Gaudet, D., Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A., Links, M.G., McCarthy, E.L., Monroy, A., Musak, I., Nilsson, D., Penniket, C., Roach, J.L. and Sarhan, F.
 Functional Genomics of Abiotic Stress in Wheat and Canola Crops

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Xenopus; Silurana.
TITLE A physical map of the *Xenopus tropicalis* genome
JOURNAL Unpublished (2003)
COMMENT Contact: Richard K Wilson
 Genome Sequencing Center
 Washington University School of Medicine
 Email: submit88@wustl.edu
 Insert Length: 75000 Std Error: 0.00
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 Class: BAC ends
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 1. 1164
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 /mol_type="genomic DNA"
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 /cclone_lib="CH216"
 /note="Vector: pTARBAC2.1; CHORI-216 *Xenopus tropicalis* BAC library"

FEATURES
 source
 5.3%; Score 47.2; DB 7; Length 1227;
 Best Local Similarity 47.6%; Pred. No. 0.19; Indels 0; Gaps 0;
 Matches 100; Conservative 0; Mismatches 110;

ORIGIN
 Query Match 5.3%; Score 47.2; DB 7; Length 1227;
 Best Local Similarity 47.6%; Pred. No. 0.19; Indels 0; Gaps 0;
 Matches 100; Conservative 0; Mismatches 110;

QY 632 TTGGAGAGCAGTCATGAGATGGGAGAGCTTCATCCCTCCCAAGCAGAAACGAAAAAT 691
 |||||
 Db 601 TTGGCGGGGGCGCTGGTAAAAACACAGGCTTCATCCCTCCCTCCNNNNNNAAAAA 660
 |||||
 QY 692 GGAGAGAGCAATTTGAGCCAGAGTTTGAGAAATAGATGCTTCATTTGAGAGAGTGCAC 751
 |||||
 Db 661 GAAAAAACAAAAAANAAAAAANAAAAAAGGAGAGAAAAAAGG 720
 |||||
 QY 752 ATAGATTGAAAAATACAGAAAAATAGTTTGGACAAATACATTTATCGAGCTTACAC 811
 |||||
 Db 721 GAAAAATCAANAAAAAGAAAAAANAAAAAANAAAAAANAAAAAANAAAAA 780
 |||||
 QY 812 TATTGCTTTGAGTAGAACAGAGATAGAA 841
 |||||
 Db 781 AATTAATATAAAAGATCAAAAAANAAAA 810

RESULT 7
 CNS0039R 1101 bp DNA linear GSS 03-JUN-1999
 LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #
 DEFINITION BACR08010 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
 AL063932
 VERSION AL063932.1 GI:4941789
 KEYWORDS GSS.
 SOURCE Drosophila melanogaster (fruit fly)
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 1101)

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM nucleic - nucleic search, using sw model
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5312.485 Million cell updates/sec
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Perfect score: 888
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Gapop 10.0, Gapext 1.0
Searched: 1303057 seqs, 888780828 residues
Total number of hits satisfying chosen parameters: 2606114

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	888	100.0	888	3	US-10-065-133A-57 Sequence 57, Appl
3	886.4	99.8	891	3	US-09-506-286B-50 Sequence 50, Appl
4	886.4	99.8	891	3	US-10-065-133A-50 Sequence 50, Appl
5	884.4	99.6	888	3	US-09-506-286B-53 Sequence 53, Appl
6	884.4	99.6	888	3	US-10-065-133A-53 Sequence 53, Appl
7	706.4	79.5	906	3	US-10-204-664A-6 Sequence 6, Appl
8	690	77.7	690	3	US-09-506-286B-52 Sequence 52, Appl
9	690	77.7	690	3	US-09-506-286B-59 Sequence 59, Appl
10	690	77.7	690	3	US-10-065-133A-52 Sequence 52, Appl
11	690	77.7	690	3	US-10-065-133A-59 Sequence 59, Appl
12	463.4	52.2	468	3	US-09-506-286B-54 Sequence 54, Appl
13	463.4	52.2	468	3	US-10-065-133A-54 Sequence 54, Appl
14	291.4	32.8	293	3	US-09-506-286B-56 Sequence 56, Appl
15	291.4	32.8	293	3	US-10-065-133A-56 Sequence 56, Appl
16	212.8	24.0	918	6	PCT-US94-01149-9 Sequence 9, Appl
17	212.8	24.0	918	6	PCT-US94-01149-58 Sequence 58, Appl
18	212	23.9	453	2	US-08-388-267C-3 Sequence 3, Appl
19	212	23.9	453	3	US-09-277-720-3 Sequence 3, Appl
20	212	23.9	690	6	PCT-US94-01149-11 Sequence 11, Appl
21	212	23.9	690	6	PCT-US94-01149-71 Sequence 71, Appl
22	212	23.9	924	6	PCT-US94-01149-15 Sequence 15, Appl
23	211.6	23.8	681	6	PCT-US94-01149-25 Sequence 25, Appl
24	211.6	23.8	717	6	PCT-US94-01149-23 Sequence 23, Appl

25	211.6	23.8	729	6	PCT-US94-01149-17 Sequence 17, Appl
26	211.6	23.8	912	6	PCT-US94-01149-31 Sequence 31, Appl
27	210.4	23.7	1014	2	US-08-441-857-7 Sequence 7, Appl
28	210.4	23.7	1014	3	US-08-193-159-7 Sequence 7, Appl
29	210.4	23.7	1014	3	US-09-283-646C-7 Sequence 7, Appl
30	210.4	23.7	1017	2	US-08-441-857-9 Sequence 9, Appl
31	210.4	23.7	1017	2	US-08-441-857-11 Sequence 11, Appl
32	210.4	23.7	1017	3	US-08-193-159-9 Sequence 9, Appl
33	210.4	23.7	1017	3	US-08-283-646C-9 Sequence 11, Appl
34	210.4	23.7	1017	3	US-09-283-646C-11 Sequence 11, Appl
35	210.4	23.7	1020	3	US-08-441-857-5 Sequence 5, Appl
36	210.4	23.7	1020	3	US-08-193-159-5 Sequence 5, Appl
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39	208.8	23.5	7616	6	PCT-US94-01149-54 Sequence 13, Appl
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41	112.6	12.7	699	6	PCT-US94-01149-21 Sequence 19, Appl
42	112	12.6	630	6	PCT-US94-01149-19 Sequence 14, Appl
43	112	12.6	810	6	PCT-US94-01149-14 Sequence 184382,
44	53.8	6.1	7218	2	US-08-232-463-14
45	42.4	4.8	601	3	US-09-949-016-184382

ALIGNMENTS

RESULT 1
US-09-506-286B-57
; Sequence 57, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; CURRENT FILING DATE: 2000-02-16
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 57
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27)..(716)
US-09-506-286B-57

Query Match	100.0%	Score 888;	DB 3;	Length 888;
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Matches 888;	Conservative 0;			
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QY	61	ACTGTTTCTTTGGCATGTCGCAAAACGATTTTCAGAGCAAGAACTGGGTGATGCCCAT	120	
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FILE REFERENCE: EQ-1-C2
CURRENT APPLICATION NUMBER: US/09/506,286B
CURRENT FILING DATE: 2000-02-16
PRIOR APPLICATION NUMBER: 09/133,921
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: PCT/US99/18583
PRIOR FILING DATE: 1999-08-12
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 50
LENGTH: 891
TYPE: DNA
ORGANISM: Equine influenza virus H3N8
FEATURE:
NAME/KEY: CDS
LOCATION: (27)..(716)
US-09-506-286B-50

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Best Local Similarity 99.9%; Pred. No. 6.7e-252;
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QY	241	AATCAGATGAGGCACTTAAATGACCAATTCCTTCTGCTTCTGCTTCTGCTTCTGCTT	300
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DB	301	ACATGACTCTTGGATGTGTCAGAGACTGGTTCATGCTCATGCTCATGCTCATGCTCATG	360
QY	361	CAGCTCCCTATGATTAAGATGACAGCAATCATGATGATGATGATGATGATGATGATGAT	420
DB	361	CAGCTCCCTATGATTAAGATGACAGCAATCATGATGATGATGATGATGATGATGATGAT	420
QY	421	CAAACTTTAGTGTGATTTTGAAGGCTGAGACATTAATTAATTAATTAATTAATTAATTA	480
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QY 781 GAACAATAACATTATTATGCAAGCCTTACAACTATTGCTTGAAGTAGAACAAGAGATAAGA 840
DB 781 GAACAATAACATTATTATGCAAGCCTTACAACTATTGCTTGAAGTAGAACAAGAGATAAGA 840
QY 841 ACTTCTCTGCTTTCAGCTTATTATGATATATAAACAACACCTTGTCTTA 888
DB 841 ACTTCTCTGCTTTCAGCTTATTATGATATATAAACAACACCTTGTCTTA 888

RESULT 4
US-10-065-133A-50
Sequence 50, Application US/10065133A
Patent No. 6685946
GENERAL INFORMATION:
APPLICANT: Dowling, Patricia W.
APPLICANT: Youngner, Julius S.
TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
FILE REFERENCE: EQ-1-C2-1
CURRENT APPLICATION NUMBER: US/10/065,133A
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: PCT/US99/18583
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 09/133,921
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn version 3.1
SEQ ID NO 50
LENGTH: 891
TYPE: DNA
ORGANISM: Equine influenza virus H3N8
FEATURE:
NAME/KEY: CDS
LOCATION: (27)..(716)
OTHER INFORMATION:
US-10-065-133A-50

Query Match 99.8%; Score 886.4; DB 3; Length 891;
Best Local Similarity 99.9%; Pred. No. 6.7e-252;
Matches 887; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	AGCAAAAGCAGGGTGACAAAACATATCGATTCCACACCTGTGTCAAGCTTTCAGGTAG	60
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DB	121	TCCTGACCGGCTTGGCGGACGACAGACTCCCTAAAGGAGAGGTAGTCTTGGTC	180
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DB	181	TGACATCGAAACAGCCACTCTGTCAGGAGACAGATAGTGGAGAGGTAGTCTTGGTC	240
QY	241	AATCAGATGAGGCACTTAAATGACCAATTCCTTCTGCTTCTGCTTCTGCTTCTGCTT	300
DB	241	AATCAGATGAGGCACTTAAATGACCAATTCCTTCTGCTTCTGCTTCTGCTTCTGCTT	300
QY	301	ACATGACTCTTGGATGTGTCAGAGACTGGTTCATGCTCATGCTCATGCTCATGCTCATG	360
DB	301	ACATGACTCTTGGATGTGTCAGAGACTGGTTCATGCTCATGCTCATGCTCATGCTCATG	360
QY	361	CAGCTCCCTATGATTAAGATGACAGCAATCATGATGATGATGATGATGATGATGATGAT	420
DB	361	CAGCTCCCTATGATTAAGATGACAGCAATCATGATGATGATGATGATGATGATGATGAT	420
QY	421	CAAACTTTAGTGTGATTTTGAAGGCTGAGACATTAATTAATTAATTAATTAATTAATTA	480
DB	421	CAAACTTTAGTGTGATTTTGAAGGCTGAGACATTAATTAATTAATTAATTAATTAATTA	480

Wed Mar 8 09:11:18 2006

481 AAGAAGGAGCAGTGGTGGGAAATTTCAACATTTGCTTCTCTCCAGGACATACATG 540
Db 481 AAGAAGGAGCAGTGGTGGGAAATTTCAACATTTGCTTCTCTCCAGGACATACATG 540
Qy 541 AGGATGTCAGAAATGCAATTTGGGTCCTCATCGGAGGACTTAAATGGAATGATACGG 600
Db 541 AGGATGTCAGAAATGCAATTTGGGTCCTCATCGGAGGACTTAAATGGAATGATACGG 600
Qy 601 TTAGAAATCTCTGAACTCTACAGAGATTCGTTGGAGAAAGCAATTCAGGAGAGTGGAGAC 660
Db 601 TTAGAAATCTCTGAACTCTACAGAGATTCGTTGGAGAAAGCAATTCAGGAGAGTGGAGAC 660
Qy 661 CTTCAATTCCTCCAAAGCAGAAACGAAATATGAGAGAAATTCAGGAGAGTGGAGT 720
Db 661 CTTCAATTCCTCCAAAGCAGAAACGAAATATGAGAGAAATTCAGGAGAGTGGAGT 720
Qy 721 GAAATAGATGGTTGATTGAAGAGTGGGACATAGATTGAAATATACAGAAATPAGTTT 780
Db 721 GAAATAGATGGTTGATTGAAGAGTGGGACATAGATTGAAATATACAGAAATPAGTTT 780
Qy 781 GACAAATACATTTATGCAAGCTTTACAACTATTGCTTGAAGTAGAGCAAGAGATAAGA 840
Db 781 GACAAATACATTTATGCAAGCTTTACAACTATTGCTTGAAGTAGAGCAAGAGATAAGA 840
Qy 841 ACTTCTGTTTCAGCTTATTAAATGATAAAACACCCCTTGTCTTA 888
Db 841 ACTTCTGTTTCAGCTTATTAAATGATAAAACACCCCTTGTCTTA 888

RESULT 5
US-09-506-286B-53
; Sequence 53, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; PRIOR FILING DATE: 2000-04-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 53
; TYPE: DNA
; LENGTH: 888
; ORGANISM: Equine influenza virus H3N8
US-09-506-286B-53

Query Match 99.6%; Score 884.4; DB 3; Length 888;
Best Local Similarity 99.9%; Pred. No. 2.6e-251;
Matches 885; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CAAAAGCAGGTCACAAAACATAATGGATTCCAAACACTGTGTCAAGCTTCAGGTAGAC 62
Db 1 CAAAAGCAGGTCACAAAACATAATGGATTCCAAACACTGTGTCAAGCTTCAGGTAGAC 60
Qy 63 TGTGTTCTTTGGCATGTTCGCAACGATTTGCAACAAAGCACTGGGTGATGCCCATTC 122
Db 61 TGTGTTCTTTGGCATGTTCGCAACGATTTGCAACAAAGCACTGGGTGATGCCCATTC 120
Qy 123 CTTGACCGGCTTCGCCGAGACAGAGTCCCTTAAAGGAGAGGTAGACATCTTTGGTCTG 182
Db 121 CTTGACCGGCTTCGCCGAGACAGAGTCCCTTAAAGGAGAGGTAGACATCTTTGGTCTG 180
Qy 183 GACATCGAAACAGGCACTCGTCGAGGAAAGCAGATAGTGGAGAGATCTCGAAGAGGAA 242
Db 181 GACATCGAAACAGGCACTCGTCGAGGAAAGCAGATAGTGGAGAGATCTCGAAGAGGAA 240

Qy 243 TCAGATGAGGACCTTAAAAATGACCAATTTGCTTCTGTTCTTCCGCTTCAAGCTTAACTGAC 302
Db 241 TCAGATGAGGACCTTAAAAATGACCAATTTGCTTCTGTTCTTCCGCTTCAAGCTTAACTGAC 300
Qy 303 ATGACTCTTGATGAGATGTCAAGAGACTGGTTCATGCTCATGCCAGCAGAAAGTAACA 362
Db 301 ATGACTCTTGATGAGATGTCAAGAGACTGGTTCATGCTCATGCCAGCAGAAAGTAACA 360
Qy 363 GGCTCCCTTATGATAAGAAATGGACCAAGCAATCATGGATAAGAAACATCATCTTAAAGCA 422
Db 361 GGCTCCCTTATGATAAGAAATGGACCAAGCAATCATGGATAAGAAACATCATCTTAAAGCA 420
Qy 423 AACTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATACTACTTTAGAGCCTTCAACGAA 482
Db 421 AACTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATACTACTTTAGAGCCTTCAACGAA 480
Qy 483 GAGGAGCAGTGGTGGCGAAATTTCACTTTCCTTCCAGGACATACATACTAATGAG 542
Db 481 GAGGAGCAGTGGTGGCGAAATTTCACTTTCCTTCCAGGACATACATACTAATGAG 540
Qy 543 GATGCAAAATGCAATTTGGGTCCTCATCGGAGACTTAAATGGAATGATAATACCGTT 602
Db 541 GATGCAAAATGCAATTTGGGTCCTCATCGGAGACTTAAATGGAATGATAATACCGTT 600
Qy 603 AGAATCTCTGAACTCTTACAGAGATTCGCTTGGAGAGCAGTCAATGAGAAATGGAGACCT 662
Db 601 AGAATCTCTGAACTCTTACAGAGATTCGCTTGGAGAGCAGTCAATGAGAAATGGAGACCT 660
Qy 663 TCATTCCTCCAAAGCAGAAACGAAATTTGAGAGAAATTTGAGGCAAGCAATTTGAGGCAAG 722
Db 661 TCATTCCTCCAAAGCAGAAACGAAATTTGAGAGAAATTTGAGGCAAGCAATTTGAGGCAAG 720
Qy 723 AATAAGATGTTGATTGAGAGAGTGGAGACATAGATTGAAATATACAGAAATAGTTTGA 782
Db 721 AATAAGATGTTGATTGAGAGAGTGGAGACATAGATTGAAATATACAGAAATAGTTTGA 780
Qy 783 ACAATAACATTTATGAGGCTTCAACTATTCCTTCAAGTGAACAGAGATAAGAAC 842
Db 781 ACAATAACATTTATGAGGCTTCAACTATTCCTTCAAGTGAACAGAGATAAGAAC 840
Qy 843 TTTCTGTTTCAGCTTATTAAATGATAAAACACCCCTTGTCTTA 888
Db 841 TTTCTGTTTCAGCTTATTAAATGATAAAACACCCCTTGTCTTA 886

RESULT 6
US-10-065-133A-53
; Sequence 53, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 53
; TYPE: DNA
; LENGTH: 888
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-53

Query Match 99.6%; Score 884.4; DB 3; Length 888;
Best Local Similarity 99.9%; Pred. No. 2.6e-251;
Matches 885; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CAAAAGCAGGTCACAAAACATAATGGATTCCAAACACTGTGTCAAGCTTCAGGTAGAC 62

Db 1 CAAAAGCAGGGTGACAAAACATGATGATTCACACATGTTCAAGCTTTTCAGGTAGAC 60
Qy 63 TGTTCCTTTTGGCATGTCGCAAAACATTTGAGACCAAGAACTGGGTGATGCCCAATTC 122
Db 61 TGTTCCTTTTGGCATGTCGCAAAACATTTGAGACCAAGAACTGGGTGATGCCCAATTC 120
Qy 123 CTTGACCGCTTCGCGAGACCGAAGTCCCTTAAGAGAGAGGTAGACCTCTTGGTCTG 182
Db 121 CTTGACCGCTTCGCGAGACCGAAGTCCCTTAAGAGAGAGGTAGACCTCTTGGTCTG 180
Qy 183 GACATCGAAACAGCCTCTGTCGAGGAAAGAGATGATGGAGAGAGATTCGGAAGAGAA 242
Db 181 GACATCGAAACAGCCTCTGTCGAGGAAAGAGATGATGGAGAGAGATTCGGAAGAGAA 240
Qy 243 TCAGATGAGGCACTTAAAGATGACCATTTGCTCTGTTCTCTTTCAGCTACTTAACCTGAC 302
Db 241 TCAGATGAGGCACTTAAAGATGACCATTTGCTCTGTTCTCTTTCAGCTACTTAACCTGAC 300
Qy 303 ATGACTCTTGATGATGTCAGAGAGACTGTTTCATGCTCATGCCCAAGCAGAAAGTAACA 362
Db 301 ATGACTCTTGATGATGTCAGAGAGACTGTTTCATGCTCATGCCCAAGCAGAAAGTAACA 360
Qy 363 GGTCTCCATGTAAGATGAGAGAGGCAATCATGATTAAGACATCTACTTAAGCA 422
Db 361 GGTCTCCATGTAAGATGAGAGAGGCAATCATGATTAAGACATCTACTTAAGCA 420
Qy 423 AACTTTAGTGTGATTTGAAAGGCTGGAGACACTAATACTACTTTAGAGCCTTCAACGAA 482
Db 421 AACTTTAGTGTGATTTGAAAGGCTGGAGACACTAATACTACTTTAGAGCCTTCAACGAA 480
Qy 483 GAAGAGAGAGTCTGTTGGCGAAATTTCAACATTTGCTCTCTTCCAGGACATACTAATGAG 542
Db 481 GAAGAGAGAGTCTGTTGGCGAAATTTCAACATTTGCTCTCTTCCAGGACATACTAATGAG 540
Qy 543 GATGTCAAAATGCAATTTGGGTCCTCATCGGAGAGCTTAAATGGAATGATTAACGTT 602
Db 541 GATGTCAAAATGCAATTTGGGTCCTCATCGGAGAGCTTAAATGGAATGATTAACGTT 600
Qy 603 AGAATCTGTAAGCTTACAGAGATTCGCTTGGAGAGAGCTCATGAGATGGAGACCT 662
Db 601 AGAATCTGTAAGCTTACAGAGATTCGCTTGGAGAGAGCTCATGAGATGGAGACCT 660
Qy 663 TCATTCCTTCCAAAGCAGAAACGAAATGGAGAGAAATGAGCCAGAGTTTGAAGA 722
Db 661 TCATTCCTTCCAAAGCAGAAACGAAATGGAGAGAAATGAGCCAGAGTTTGAAGA 720
Qy 723 AATAAGATGTTGATTTGAAGAAGTGCGACATAGATTGAAAAATACAGAAAAATAGTTTGA 782
Db 721 AATAAGATGTTGATTTGAAGAAGTGCGACATAGATTGAAAAATACAGAAAAATAGTTTGA 780
Qy 783 ACAAATACATTTATGCAAGCTTACAACTATGCTTGAAGTAGAGAGAGATTAAGAC 842
Db 781 ACAAATACATTTATGCAAGCTTACAACTATGCTTGAAGTAGAGAGAGATTAAGAC 840
Qy 843 TTTCTGTTTACGCTTATTAATGATTAAGAAAAACCCCTTGTCTTA 888
Db 841 TTTCTGTTTACGCTTATTAATGATTAAGAAAAACCCCTTGTCTTA 886

RESULT 7

US-10-204-664A-6
; Sequence 6, Application US/10204664A
; Patent No. 6800288
; GENERAL INFORMATION:
; APPLICANT: FERKO, Boris
; APPLICANT: EGOROV, Andre
; APPLICANT: VOGLAUER, Regina
; TITLE OF INVENTION: Recombinant Influenza A Viruses
; FILE REFERENCE: 113529
; CURRENT APPLICATION NUMBER: US/10/204,664A
; CURRENT FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: EP 00104338.9

; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 906
; TYPE: DNA
; ORGANISM: Influenza A virus /PRNS38
US-10-204-664A-6

Query Match 79.5%; Score 706.4; DB 3; Length 906;
Best Local Similarity 88.2%; Pred. No. 1.2e-198;
Matches 797; Conservative 0; Mismatches 91; Indels 16; Gaps 2;

Qy 1 AGCAAAAGCAGGGTGACAAAACATTAATGGATTCCAACTGTGTCAAGCTTTTCAGGTAG 60
Db 1 AGCAAAAGCAGGGTGACAAAACATTAATGGATTCCAACTGTGTCAAGCTTTTCAGGTAG 60
Qy 61 ACTGTTTCTTTGGCATGTCGCAAAACGATTTGAGACCAAGAACTGGGTGATGCCCAT 120
Db 61 ATTGCTTCTTTGGCATGTCGCAAAACGATTTGAGACCAAGAACTGGGTGATGCCCAT 120
Qy 121 TCCTTCACCGGCTTCGCGAG-----ACGAGAGTCCCTAAAGGAAG 165
Db 121 TCCTTCACCGGCTTCGCGAGTGAATACTAGCTGATCAGAAATCCTTAAGGAAGGG 180
Qy 166 GTAGCACTCTTGGTCTGGAATCGAAACAGCCACTGTCGAGGAAAGCAGATAGTGGAGC 225
Db 181 GCAGCACTCTTGGTCTGGAATCGGAATCGAGACCAAGCACTGTCGGAAGCAGATAGTGGAGC 240
Qy 226 AGATTCGAGAGAGAGATTCAGATGAGGCACTTAAATGACCAATGCTGTCTGTCTCTGTT 285
Db 241 GGAATCTGAAAGAGAAATCCGATGAGGCACTTAAATGACCAATGCTGTCTGTCTGTT 300
Qy 286 CAGCTACTTAACTGACATGACTCTTGTGATGATGTCAGAGACTGTTTCATGCTCATGC 345
Db 301 CGGCTTACCTAATGACATGACTCTTGTGAGAAATGTCAGGAGTGTCCATGCTCATAC 360
Qy 346 CCAGCAGAAAGTAAAGTCCCTCTATGTAAGAAAGCAGGAGGCAAGCAATCATGGA- TAAG 404
Db 361 CCAGCAGAAAGTAAAGTCCCTCTTGTATGTAAGAAAGCAGGAGGCAATCATGGA- TAAG 420
Qy 405 AACATCATCTTAAAGCAAACTTTAGTGTGATTTTGAAGGCTGGAGACACTAATACTA 464
Db 421 AACATCATCTTAAAGCAAACTTTAGTGTGATTTTGAAGGCTGGAGACACTAATACTA 480
Qy 465 CTTAGAGCCTTCCAGGAGAGGAGCAGTCTGTTGGCGAAATTTTCCACATTTGCTCTCTT 524
Db 481 CTAAGGCTTTTCCAGGAGAGGAGCAATTTGTTGGCGAAATTTTCCACATTTGCTCTCTT 540
Qy 525 CCAGGACATCTAATGAGAGATGTCAAAATGCAATTTGGGGTCTCTCATCGAGAGACTTAAA 584
Db 541 CCAGGACATCTAATGAGAGATGTCAAAATGCAATTTGGGGTCTCTCATCGAGAGACTTAAA 600
Qy 585 TGAATCATTAATACGGTTAGAACTCTGAACTCTACAGATTCGCTTGGAGAGAGCT 644
Db 601 TGAATCATTAATACGGTTAGAACTCTGAACTCTACAGATTCGCTTGGAGAGAGCT 660
Qy 645 CATGAGATGGAGACCTTCAATTCCTCCAAAGCAGAAACGAAATTAAGAGAGAACTTAA 704
Db 661 AATGAGATGGAGACCTTCAATTCCTCCAAAGCAGAAACGAGAAATGGCGGAGCAAT 720
Qy 705 GAGCAGAAATTTGAAGAAATTAAGATGTTGATTAAGAGAGTGCATAGATTGAAAAA 764
Db 721 AGGTCAGAAATTTGAAGAAATTAAGATGTTGATTAAGAGAGTGCATAGATTGAAAAA 780
Qy 765 TACAGAAATAGTTTGAAGAAATTAAGATGTTGATTAAGAGAGTGCATAGATTGAAAAA 824
Db 781 AACAGAGATAGTTTGAAGAAATTAAGATGTTGATTAAGAGAGTGCATAGATTGAAAAA 840
Qy 825 AGAACAAGATAGAACTTCTGCTTTCAGCTTATTAATGATTAAGAAACACCCCTTGT 884
Db 841 GGAGCAAGAGATAGAACTTCTGCTTTCAGCTTATTAATGATTAAGAAACACCCCTTGT 900

us-10-734-373-57.rni

Wed Mar 8 09:11:18 2006

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Qy 885 TCTA 888
Db 901 TCTA 904

RESULT 8
US-09-506-286B-52
; Sequence 52, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-09-506-286B-52

Query Match 77.7%; Score 690; DB 3; Length 690;
Best Local Similarity 100.0%; Pred. No. 7.5e-194;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ATGGATTCCAAACACTGCTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATCTCGCAAA 86
Db 1 ATGGATTCCAAACACTGCTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATCTCGCAAA 60

Qy 87 CGATTTCGACCAAGAACTGGGTGATGCCCATTCCTTGACCGGCTTCGCCGAGACCAAG 146
Db 61 CGATTTCGACCAAGAACTGGGTGATGCCCATTCCTTGACCGGCTTCGCCGAGACCAAG 120

Qy 147 AAGTCCCTTAAAGAGAGGTAGACACTTTGGTCTGGACATCGAAACAGCCACTCTGTGCA 206
Db 121 AAGTCCCTTAAAGAGAGGTAGACACTTTGGTCTGGACATCGAAACAGCCACTCTGTGCA 180

Qy 207 GGAAGCAGATAGTGGAGCAGATTCGGAAGAGGAATCAGATGAGGCACTTAAATGACC 266
Db 181 GGAAGCAGATAGTGGAGCAGATTCGGAAGAGGAATCAGATGAGGCACTTAAATGACC 240

Qy 267 ATTGCTCTGTTCTGCTTCAAGCTTAACTGACATGACTCTTTGATGAGATGTCAGAA 326
Db 241 ATTGCTCTGTTCTGCTTCAAGCTTAACTGACATGACTCTTTGATGAGATGTCAGAA 300

Qy 327 GACTGGTTTCATGCTCATGCCAAGCAGAAAGTAAACAGGCTCCCTATGTATGAAGATGGAC 386
Db 301 GACTGGTTTCATGCTCATGCCAAGCAGAAAGTAAACAGGCTCCCTATGTATGAAGATGGAC 360

Qy 387 CAGGCAATCATGGAATGAACATCATCTTAAAGCAACTTTAGTGTGATTTTCAAAAGG 446
Db 361 CAGGCAATCATGGAATGAACATCATCTTAAAGCAACTTTAGTGTGATTTTCAAAAGG 420

Qy 447 CTGGAGACA CTAATACTACTTAGAGCTTCAAGAGAGGAGGAGCTGTTGGGCAATT 506
Db 421 CTGGAGACA CTAATACTACTTAGAGCTTCAAGAGAGGAGGAGCTGTTGGGCAATT 480

Qy 507 TCACCAATGCTCTCTCTTCAGGACATTAATGAGATGATCGTTGAGATCTCAAGAG 566
Db 481 TCACCAATGCTCTCTCTTCAGGACATTAATGAGATGATCGTTGAGATCTCAAGAG 540

Qy 567 CTCATCGGAGGACTTAAATGGAATGATTAATGAGATGATCGTTGAGATCTCAAGAG 626
Db 541 CTCATCGGAGGACTTAAATGGAATGATTAATGAGATGATCGTTGAGATCTCAAGAG 600

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Qy 627 TTCGCTTGGAGAGAGCATGATGAGAAATGGAGACCTTCAATTCCTCCAAAGCAGAAACGA 686
Db 601 TTCGCTTGGAGAGAGCATGATGAGAAATGGAGACCTTCAATTCCTCCAAAGCAGAAACGA 660

Qy 687 AAAATGGAGAGAAACAAATTGAGCCAGAGTTT 716
Db 661 AAAATGGAGAGAAACAAATTGAGCCAGAGTTT 690

RESULT 9
US-09-506-286B-59
; Sequence 59, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-09-506-286B-59

Query Match 77.7%; Score 690; DB 3; Length 690;
Best Local Similarity 100.0%; Pred. No. 7.5e-194;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ATGGATTCCAAACACTGCTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCGCAAA 86
Db 1 ATGGATTCCAAACACTGCTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCGCAAA 60

Qy 87 CGATTTCGACCAAGAACTGGGTGATGCCCATTCCTTGACCGGCTTCGCCGAGACCAAG 146
Db 61 CGATTTCGACCAAGAACTGGGTGATGCCCATTCCTTGACCGGCTTCGCCGAGACCAAG 120

Qy 147 AAGTCCCTTAAAGAGAGGTAGACACTTTGGTCTGGACATCGAAACAGCCACTCTGTGCA 206
Db 121 AAGTCCCTTAAAGAGAGGTAGACACTTTGGTCTGGACATCGAAACAGCCACTCTGTGCA 180

Qy 207 GGAAGCAGATAGTGGAGCAGATTCGGAAGAGGAATCAGATGAGGCACTTAAATGACC 266
Db 181 GGAAGCAGATAGTGGAGCAGATTCGGAAGAGGAATCAGATGAGGCACTTAAATGACC 240

Qy 267 ATTGCTCTGTTCTGCTTCAAGCTTAACTGACATGACTCTTTGATGAGATGTCAGAA 326
Db 241 ATTGCTCTGTTCTGCTTCAAGCTTAACTGACATGACTCTTTGATGAGATGTCAGAA 300

Qy 327 GACTGGTTTCATGCTCATGCCAAGCAGAAAGTAAACAGGCTCCCTATGTATGAAGATGGAC 386
Db 301 GACTGGTTTCATGCTCATGCCAAGCAGAAAGTAAACAGGCTCCCTATGTATGAAGATGGAC 360

Qy 387 CAGGCAATCATGGAATGAACATCATCTTAAAGCAACTTTAGTGTGATTTTCAAAAGG 446
Db 361 CAGGCAATCATGGAATGAACATCATCTTAAAGCAACTTTAGTGTGATTTTCAAAAGG 420

Qy 447 CTGGAGACA CTAATACTACTTAGAGCTTCAAGAGAGGAGGAGCTGTTGGGCAATT 506
Db 421 CTGGAGACA CTAATACTACTTAGAGCTTCAAGAGAGGAGGAGCTGTTGGGCAATT 480

Qy 507 TCACCAATGCTCTCTCTTCAGGACATTAATGAGATGATCGTTGAGATCTCAAGAG 566
Db 481 TCACCAATGCTCTCTCTTCAGGACATTAATGAGATGATCGTTGAGATCTCAAGAG 540

Qy 567 CTCATCGGAGGACTTAAATGGAATGATTAATGAGATGATCGTTGAGATCTCAAGAG 626
Db 541 CTCATCGGAGGACTTAAATGGAATGATTAATGAGATGATCGTTGAGATCTCAAGAG 600

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QY 567 CTATCGGAGGACTTAATGAATGATATACGGTTAGAATCTCTGAACTCTACAGAGA 626
DB 541 CTATCGGAGGACTTAATGAATGATATACGGTTAGAATCTCTGAACTCTACAGAGA 600
QY 627 TTGCTTGGAGAGCAGTCATGAGATGGAGACCTTCATTCCTCCAAAGCAGAAACGA 686
DB 601 TTGCTTGGAGAGCAGTCATGAGATGGAGACCTTCATTCCTCCAAAGCAGAAACGA 660
QY 687 AAATCGAGAGAACAAATTGAGCCAGAGTT 716
DB 661 AAATCGAGAGAACAAATTGAGCCAGAGTT 690

RESULT 10

US-10-065-133A-52
; Sequence 52, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 52
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-52

Query Match 77.7%; Score 690; DB 3; Length 690;
Best Local Similarity 100.0%; Pred. No. 7.5e-194;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ATGGATTCCACACTGTGTCAAGCTTTCAGGTAGACTGTTCTTTGGCGAATGTCGCAAA 86
DB 1 ATGGATTCCACACTGTGTCAAGCTTTCAGGTAGACTGTTCTTTGGCGAATGTCGCAAA 60
QY 87 CGATTTTCGAGACCAAGAACTGGGTGATGCCCATTCCTTGACCGGCTTCGCGAGACGAG 146
DB 61 CGATTTTCGAGACCAAGAACTGGGTGATGCCCATTCCTTGACCGGCTTCGCGAGACGAG 120
QY 147 AAGTCCCTTAAAGGAGAGGTAGTACCTCTTGGTCTGGACATCGAAACAGCCACTCGTGCA 206
DB 121 AAGTCCCTTAAAGGAGAGGTAGTACCTCTTGGTCTGGACATCGAAACAGCCACTCGTGCA 180
QY 207 GGAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGCACTTAAATGACC 266
DB 181 GGAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGCACTTAAATGACC 240
QY 267 ATTGCCTCTGTTCTGCTTCAAGCTTAACTGATGATGATGATGATGATGATGATGATGAT 326
DB 241 ATTGCCTCTGTTCTGCTTCAAGCTTAACTGATGATGATGATGATGATGATGATGATGAT 300
QY 327 GACTGTTTCACTCATGCCCAAGCAATCACTTAAAGCAAACTTAAAGCAAACTTAAAGCAAA 386
DB 301 GACTGTTTCACTCATGCCCAAGCAATCACTTAAAGCAAACTTAAAGCAAACTTAAAGCAAA 360
QY 387 CAGGCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 446
DB 361 CAGGCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 447 CTGGAGACATAACTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTT 506
DB 421 CTGGAGACATAACTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTT 480
QY 507 TCACCATTCCTCTCTTCAGGACATACATAATGAGGATGTCAAAATGCAATGGGGTC 566

DB 481 TCACCATTCCTCTCTTCAGGACATACATAATGAGGATGTCAAAATGCAATGGGGTC 540
QY 567 CTATCGGAGGACTTAATGAATGATATACGGTTAGAATCTCTGAACTCTACAGAGA 626
DB 541 CTATCGGAGGACTTAATGAATGATATACGGTTAGAATCTCTGAACTCTACAGAGA 600
QY 627 TTGCTTGGAGAGCAGTCATGAGATGGAGACCTTCATTCCTCCAAAGCAGAAACGA 686
DB 601 TTGCTTGGAGAGCAGTCATGAGATGGAGACCTTCATTCCTCCAAAGCAGAAACGA 660
QY 687 AAATCGAGAGAACAAATTGAGCCAGAGTT 716
DB 661 AAATCGAGAGAACAAATTGAGCCAGAGTT 690

RESULT 11

US-10-065-133A-59
; Sequence 59, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 59
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-59

Query Match 77.7%; Score 690; DB 3; Length 690;
Best Local Similarity 100.0%; Pred. No. 7.5e-194;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ATGGATTCCACACTGTGTCAAGCTTTCAGGTAGACTGTTCTTTGGCGAATGTCGCAAA 86
DB 1 ATGGATTCCACACTGTGTCAAGCTTTCAGGTAGACTGTTCTTTGGCGAATGTCGCAAA 60
QY 87 CGATTTTCGAGACCAAGAACTGGGTGATGCCCATTCCTTGACCGGCTTCGCGAGACGAG 146
DB 61 CGATTTTCGAGACCAAGAACTGGGTGATGCCCATTCCTTGACCGGCTTCGCGAGACGAG 120
QY 147 AAGTCCCTTAAAGGAGAGGTAGTACCTCTTGGTCTGGACATCGAAACAGCCACTCGTGCA 206
DB 121 AAGTCCCTTAAAGGAGAGGTAGTACCTCTTGGTCTGGACATCGAAACAGCCACTCGTGCA 180
QY 207 GGAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGCACTTAAATGACC 266
DB 181 GGAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGCACTTAAATGACC 240
QY 267 ATTGCCTCTGTTCTGCTTCAAGCTTAACTGATGATGATGATGATGATGATGATGATGAT 326
DB 241 ATTGCCTCTGTTCTGCTTCAAGCTTAACTGATGATGATGATGATGATGATGATGATGAT 300
QY 327 GACTGTTTCACTCATGCCCAAGCAATCACTTAAAGCAAACTTAAAGCAAACTTAAAGCAAA 386
DB 301 GACTGTTTCACTCATGCCCAAGCAATCACTTAAAGCAAACTTAAAGCAAACTTAAAGCAAA 360
QY 387 CAGGCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 446
DB 361 CAGGCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
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Db 421 CTGGAGACATAAATACTACTTAGAGCCTTCAACGAAAGAGGACAGTCTGTTGCGAAATT 480
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Db 481 TCACCAATTCGCTTCTCTCCAGGACATATAAATGAGGATGTCAAAATGCAATTTGGGTC 540
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Qy 627 TTCGCTTCGAGAGCAGTCAATGAGAAATGGGAGACCTTCATTCCTCCAAAGCAGAAACGA 686
Db 601 TTCGCTTCGAGAGCAGTCAATGAGAAATGGGAGACCTTCATTCCTCCAAAGCAGAAACGA 660
Qy 687 AAATGAGAGAGCAATTTGAGCCAGAAGTT 716
Db 661 AAATGAGAGAGCAATTTGAGCCAGAAGTT 690

RESULT 12
US-09-506-286B-54
; Sequence 54, Application US/09506286B
; Patent No. 8482410
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Younger, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 54
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(293)
US-09-506-286B-54

Query Match 52.2%; Score 463.4; DB 3; Length 468;
Best Local Similarity 99.8%; Pred. No. 6.6e-127;
Matches 464; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 424 ACTTTAGTGTGATTTTCGAAAGGCTGGAGACATACTACTTAGAGCCTTCACCGAAG 483
Db 1 ACTTTAGTGTGATTTTCGAAAGGCTGGAGACATACTACTTAGAGCCTTCACCGAAG 60
Qy 484 AAGGAGCAGTCTGTTGGCGAAATTTCAACATTCGCTTCTCCAGGACATTAATGAGG 543
Db 61 AAGGAGCAGTCTGTTGGCGAAATTTCAACATTCGCTTCTCCAGGACATTAATGAGG 120
Qy 544 ATGTCAAAAATGCAATTTGGGGTCTCATCGAGAGCTTAAATGGAATGATTAACGGTTA 603
Db 121 ATGTCAAAAATGCAATTTGGGGTCTCATCGAGAGCTTAAATGGAATGATTAACGGTTA 180
Qy 604 GAATCTCTGAAACTCTACAGAGATTCGCTTGGAGAGCAGTCAATGAGAAATGGGACCTT 663
Db 181 GAATCTCTGAAACTCTACAGAGATTCGCTTGGAGAGCAGTCAATGAGAAATGGGACCTT 240
Qy 664 CATTCCTCCAAAGCAGAAACGAAAAATGGAGAGAACAAATGGAGCAGAGTTTGAAGAA 723
Db 241 CATTCCTCCAAAGCAGAAACGAAAAATGGAGAGAACAAATGGAGCAGAGTTTGAAGAA 300
Qy 724 ATAAGATGGTTGATTTGAAGAAGTGGCGACATAGATTGAAAAATACAGAAATAGTTTGA 783
Db 301 ATAAGATGGTTGATTTGAAGAAGTGGCGACATAGATTGAAAAATACAGAAATAGTTTGA 360

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Qy 844 TTCTCGTTTCAGCTTATTTAATGATAAAAAACACCCCTTCTTTCTA 888
Db 421 TTCTCGTTTCAGCTTATTTAATGATAAAAAACACCCCTTCTTTCTA 465

RESULT 13
US-10-065-133A-54
; Sequence 54, Application US/10065133A
; Patent No. 6895946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Younger, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 54
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(293)
; OTHER INFORMATION:
US-10-065-133A-54

Query Match 52.2%; Score 463.4; DB 3; Length 468;
Best Local Similarity 99.8%; Pred. No. 6.6e-127;
Matches 464; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 424 ACTTTAGTGTGATTTTCGAAAGGCTGGAGACATACTACTTAGAGCCTTCACCGAAG 483
Db 1 ACTTTAGTGTGATTTTCGAAAGGCTGGAGACATACTACTTAGAGCCTTCACCGAAG 60
Qy 484 AAGGAGCAGTCTGTTGGCGAAATTTCAACATTCGCTTCTCCAGGACATTAATGAGG 543
Db 61 AAGGAGCAGTCTGTTGGCGAAATTTCAACATTCGCTTCTCCAGGACATTAATGAGG 120
Qy 544 ATGTCAAAAATGCAATTTGGGGTCTCATCGAGAGCTTAAATGGAATGATTAACGGTTA 603
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RESULT 14

US-09-506-286B-56
; Sequence 56, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 293
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-09-506-286B-56

Query Match 32.8%; Score 291.4; DB 3; Length 293;
Best Local Similarity 99.7%; Pred. No. 4e-76; Indels 0; Gaps 0;
Matches 292; Conservative 0; Mismatches 1;
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DB 1 ACTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATACTACTTAGAGCCTTCACCGAAG 60
QY 484 AAGGAGCAGTCGTTGGCGAAATTCACCATTCGCTTCTCCAGGACATCTAATGAGG 543
DB 61 AAGGAGCAGTCGTTGGCGAAATTCACCATTCGCTTCTCCAGGACATCTAATGAGG 120
QY 544 ATGTCAAAAATGCAATTGGGGTCTCATCGGAGGACTTAAATGGAATGATATACGGTTA 603
DB 121 ATGTCAAAAATGCAATTGGGGTCTCATCGGAGGACTTAAATGGAATGATATACGGTTA 180
QY 604 GAATCTCTGAACCTCTACAGAGATTCGCTTGGAGAGCAGTCATGAGATGGAGACCTT 663
DB 181 GAATCTCTGAACCTCTACAGAGATTCGCTTGGAGAGCAGTCATGAGATGGAGACCTT 240
QY 664 CATTCCTCCAAAGCAGAAACGAAAATTCGAGAGACAAATTCAGCCAGAGTT 716
DB 241 CATTCCTCCAAAGCAGAAACGAAAATTCGAGAGACAAATTCAGCCAGAGTT 293

RESULT 15

US-10-065-133A-56
; Sequence 56, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; CURRENT APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 293
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-56

Query Match 32.8%; Score 291.4; DB 3; Length 293;
Best Local Similarity 99.7%; Pred. No. 4e-76; Indels 0; Gaps 0;
Matches 292; Conservative 0; Mismatches 1;
QY 424 ACTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATACTACTTAGAGCCTTCACCGAAG 483
DB 1 ACTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATACTACTTAGAGCCTTCACCGAAG 60
QY 484 AAGGAGCAGTCGTTGGCGAAATTCACCATTCGCTTCTCCAGGACATCTAATGAGG 543
DB 61 AAGGAGCAGTCGTTGGCGAAATTCACCATTCGCTTCTCCAGGACATCTAATGAGG 120
QY 544 ATGTCAAAAATGCAATTGGGGTCTCATCGGAGGACTTAAATGGAATGATATACGGTTA 603
DB 121 ATGTCAAAAATGCAATTGGGGTCTCATCGGAGGACTTAAATGGAATGATATACGGTTA 180
QY 604 GAATCTCTGAACCTCTACAGAGATTCGCTTGGAGAGCAGTCATGAGATGGAGACCTT 663
DB 181 GAATCTCTGAACCTCTACAGAGATTCGCTTGGAGAGCAGTCATGAGATGGAGACCTT 240
QY 664 CATTCCTCCAAAGCAGAAACGAAAATTCGAGAGACAAATTCAGCCAGAGTT 716
DB 241 CATTCCTCCAAAGCAGAAACGAAAATTCGAGAGACAAATTCAGCCAGAGTT 293

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Job time : 299.125 secs

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Title: US-10-734-373-57
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Gapop 10.0, Gapext 1.0
Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	888	100.0	888	7	US-10-734-373-57 Sequence 57, Appl
3	888	100.0	888	9	US-10-181-585B-39 Sequence 39, Appl
4	886.4	99.8	891	6	US-10-065-133A-50 Sequence 50, Appl
5	886.4	99.8	891	7	US-10-734-373-50 Sequence 50, Appl
6	886.4	99.8	891	9	US-10-181-585B-32 Sequence 32, Appl
7	884.4	99.6	888	6	US-10-065-133A-53 Sequence 53, Appl
8	884.4	99.6	888	7	US-10-734-373-53 Sequence 53, Appl
9	884.4	99.6	888	9	US-10-181-585B-35 Sequence 35, Appl
10	742.4	83.6	890	8	US-10-855-875-6 Sequence 6, Appl
11	737.6	83.1	890	7	US-10-381-530-8 Sequence 8, Appl
12	692.8	78.0	824	9	US-10-654-737-2 Sequence 2, Appl
13	690	77.7	690	6	US-10-065-133A-52 Sequence 52, Appl
14	690	77.7	690	7	US-10-065-133A-59 Sequence 59, Appl
15	690	77.7	690	7	US-10-734-373-52 Sequence 52, Appl
16	690	77.7	690	7	US-10-734-373-59 Sequence 59, Appl
17	690	77.7	690	9	US-10-181-585B-34 Sequence 34, Appl
18	690	77.7	690	9	US-10-181-585B-41 Sequence 41, Appl
19	684.8	77.1	824	9	US-10-654-737-1 Sequence 1, Appl
20	463.4	52.2	468	6	US-10-065-133A-54 Sequence 54, Appl
21	463.4	52.2	468	7	US-10-734-373-54 Sequence 54, Appl
22	463.4	52.2	468	9	US-10-181-585B-36 Sequence 36, Appl
23	291.4	32.8	293	6	US-10-065-133A-56 Sequence 56, Appl

24	291.4	32.8	293	7	US-10-734-373-56 Sequence 56, Appl
25	291.4	32.8	293	9	US-10-181-585B-38 Sequence 38, Appl
26	209.2	23.6	849	6	US-10-226-872-8 Sequence 8, Appl
27	209.2	23.6	849	6	US-10-226-872-9 Sequence 9, Appl
28	209.2	23.6	849	7	US-10-650-608-8 Sequence 8, Appl
29	209.2	23.6	849	7	US-10-650-608-9 Sequence 9, Appl
30	208.8	23.5	939	6	US-10-312-089-2 Sequence 2, Appl
31	208.8	23.5	939	6	US-10-312-089-4 Sequence 4, Appl
32	103.4	11.6	136	3	US-09-835-694-14 Sequence 14, Appl
33	47	5.3	4257	6	US-10-369-493-46002 Sequence 46002, A
34	44.2	5.0	552	7	US-10-021-323-93 Sequence 93, Appl
35	43	4.8	13361	10	US-11-097-143-24181 Sequence 24181, A
36	43	4.8	3673778	6	US-10-312-841-1 Sequence 1, Appl
37	42.6	4.7	6436	6	US-10-311-455-654 Sequence 654, Appl
38	41.6	4.7	590	5	US-10-027-632-290656 Sequence 290656, A
39	41.6	4.7	590	6	US-10-027-632-290656 Sequence 290656, A
40	41.4	4.7	640681	3	US-09-790-988-1 Sequence 1, Appl
41	41.2	4.6	647	8	US-10-425-115-40312 Sequence 40312, A
42	41.2	4.6	6076	7	US-10-221-74A-386 Sequence 386, Appl
43	41.2	4.6	217409	5	US-10-087-132-1954 Sequence 1954, Appl
44	41.2	4.6	3673778	6	US-10-312-841-1 Sequence 1, Appl
45	41	4.6	6351	6	US-10-311-455-1420 Sequence 1420, Appl

ALIGNMENTS

RESULT 1

US-10-065-133A-57
; Sequence 57, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57:
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27)..(716)
; OTHER INFORMATION:
US-10-065-133A-57

Query Match 100.0%; Score 888; DB 6; Length 888;
Best Local Similarity 100.0%; Pred. No. 3.3e-232;
Matches 888; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	ACTGTTTCTTTGGCAGTCCGCAACAGATTTCAGACCAAGACTGGGTGATGCCCAT	120
DB	61	ACTGTTTCTTTGGCAGTCCGCAACAGATTTCAGACCAAGACTGGGTGATGCCCAT	120
QY	121	TCTTTCACCGCTTTCGGCGAGACAGAACTCCCTAAAGAGAGAGTAGACTCTTGGTC	180
DB	121	TCTTTCACCGCTTTCGGCGAGACAGAACTCCCTAAAGAGAGAGTAGACTCTTGGTC	180
QY	181	TGACATCGAAACAGCCACTCTGTCAGAGAAAGACAGATGTGGAGAGAGG	240
DB	181	TGACATCGAAACAGCCACTCTGTCAGAGAAAGACAGATGTGGAGAGAGG	240

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	QY	241	AATCGAGTGGGCACTTAAATGCACATTGCTTCCTTGCTTCCGTACTTTAACTG	300
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	QY	301	ACATGACTCTTAGTCAGAGTCTCAAGAGCATGGTTTCATGCTCATGCCACGAGAAGTAA	360
	DB	301	ACATGACTCTTAGTCAGAGTCTCAAGAGCATGGTTTCATGCTCATGCCACGAGAAGTAA	360
	QY	361	CAGGCTCCCCTATGTTAAGAAATGGACACGCAANTCATGATGAAGAACATCATACTTTAAAG	420
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	QY	421	CAAACCTTTAGTGTGATTTTGGAAAGCTGGAGACA CTATATCTACTTTAGAGCTCTCACCG	480
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	QY	481	AAGAAGGAGCAGTCCGTTGGAGAAATTCACATTTGCCCTCTTCCAGHACATACTATNG	540
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	QY	541	AGGATGTCAAAAATGCMAATTCGGGTCTCATCGAGGAC TTTAAATGGAAATGATPATACGG	600
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	QY	661	CTTTCATTCCTCCNAAGCAGAAAAATGGAGAGAACAT TTGAGCCAGAA GTTTGAA	720
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	QY	841	ACTTCTCGTTTCAGCTTATTTAATGATAAAAAACAC CCGTTGTTCTTA	900
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RESULT 2
US-10-734-373-57
; Sequence 57, Application US/10734373
; Publication No. US20040137015A1
; GENERAL INFORMATION:
; APPLICANT: DOWLING, Patricia W.
; APPLICANT: DOWLING, Julius S.
; FILER REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/734,373
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ. ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ. ID NO 57
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27)..(716)
; OTHER INFORMATION:
US-10-734-373-57

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; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C3-PUS
; CURRENT APPLICATION NUMBER: US/10/181.585B
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: PCT/US01/05048
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/506,286
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27)..(716)
US-10-181-585B-39

Query Match      100.0%; Score 888; DB 9; Length 888;
Best Local Similarity 100.0%; Pred. No. 3.3e-232; Mismatches 0; Indels 0; Gaps 0;
Matches 888; Conservative 0;

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Qy 241 AATCAGATGAGGCACCTTAAATGACCAATTCGAGAGCTTAAATGGAATGATAATACGG 300
Db 241 AATCAGATGAGGCACCTTAAATGACCAATTCGAGAGCTTAAATGGAATGATAATACGG 300
Qy 301 ACATGACTCTTGAACCTTACAGAGATTCGCTTGGAGAGCAGTCAATGGAATGGAAGAC 660
Db 301 ACATGACTCTTGAACCTTACAGAGATTCGCTTGGAGAGCAGTCAATGGAATGGAAGAC 660
Qy 661 CTTCAATTCCTCCAAAGCAAGAAACGAAATGAGAGAAACAAATGAGCCAGAGATTGAA 720
Db 661 CTTCAATTCCTCCAAAGCAAGAAACGAAATGAGAGAAACAAATGAGCCAGAGATTGAA 720
Qy 721 GAAATAAGATGGTTGATGGAAGAGTGCAGATAGATTGAAATATACAGAAATAGTTTT 780

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Db 721 GAATAAGATGGTTGATGGAAGAGTGCAGATAGATTGAAATATACAGAAATAGTTTT 780
Qy 781 GAACAAATAACATTTATGCAAGCTTTACAACTATTGCTTGAAGTGAACCAAGAGATAAG 840
Db 781 GAACAAATAACATTTATGCAAGCTTTACAACTATTGCTTGAAGTGAACCAAGAGATAAG 840
Qy 841 ACTTCTCGTTTTCAGCTTATTATTAATGATAAAAAACACCCCTTGTGTTCTA 888
Db 841 ACTTCTCGTTTTCAGCTTATTATTAATGATAAAAAACACCCCTTGTGTTCTA 888

RESULT 4
US-10-065-133A-50
; Sequence 50: Application US/10065133A
; Publication No: US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 891
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27)..(716)
; OTHER INFORMATION:
US-10-065-133A-50

Query Match      99.8%; Score 896.4; DB 6; Length 891;
Best Local Similarity 99.9%; Pred. No. 9e-232;
Matches 887; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGCAAAAGCAGGGTGACAAACATATATGGATTCACAACTGTGTCAAGCTTTCAGGTAG 60
Db 1 AGCAAAAGCAGGGTGACAAACATATATGGATTCACAACTGTGTCAAGCTTTCAGGTAG 60
Qy 61 ACTGTTTTCTTTGGCATGTCCGCAACGATTTGCAGACCAAGAACTGGGTGATGCCCCAT 120
Db 61 ACTGTTTTCTTTGGCATGTCCGCAACGATTTGCAGACCAAGAACTGGGTGATGCCCCAT 120
Qy 121 TCCTTGACCGGGCTTCGCCGAGACCAAGATCCCTTAAAGGAAGAGGTAGCACTCTTGGTC 180
Db 121 TCCTTGACCGGGCTTCGCCGAGACCAAGATCCCTTAAAGGAAGAGGTAGCACTCTTGGTC 180
Qy 181 TGGACATCGAAACAGCCACTCGTGCAGGAAGCAGATAGTGGAGCAGATTCGGAAGAGG 240
Db 181 TGGACATCGAAACAGCCACTCGTGCAGGAAGCAGATAGTGGAGCAGATTCGGAAGAGG 240
Qy 241 AATCAGATGAGGCACCTTAAATGACCAATTCGAGAGCTTAAATGGAATGATAATACGG 300
Db 241 AATCAGATGAGGCACCTTAAATGACCAATTCGAGAGCTTAAATGGAATGATAATACGG 300
Qy 301 ACATGACTCTTGAACCTTACAGAGATTCGCTTGGAGAGCAGTCAATGGAATGGAAGAC 360
Db 301 ACATGACTCTTGAACCTTACAGAGATTCGCTTGGAGAGCAGTCAATGGAATGGAAGAC 360
Qy 361 CAGGCTCCCTTCCAAAGCAAGAAACGAAATGAGAGAAACAAATGAGCCAGAGATTGAA 420
Db 361 CAGGCTCCCTTCCAAAGCAAGAAACGAAATGAGAGAAACAAATGAGCCAGAGATTGAA 420
Qy 421 CAAACTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATATCTACTTAGAGCCTTACCG 480

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FEATURE:
; NAME/KEY: CDS
; LOCATION: (27)...(716)
US-10-181-585B-32

Query Match 99.8%; Score 886.4; DB 9; Length 891;
Best Local Similarity 99.9%; Pred. No. 98-232;
Matches 887; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCAAGCAGGGTGACAAAACATTAATGGATTCCACACTGTGTCAAGCTTTTCAGTAG 60
DB 1 AGCAAGCAGGGTGACAAAACATTAATGGATTCCACACTGTGTCAAGCTTTTCAGTAG 60
QY 61 ACTGTTTCTTTGGCATGTCCGCAACGATTTGCAGACCAAGAACTGGGTGATGCCCAT 120
DB 61 ACTGTTTCTTTGGCATGTCCGCAACGATTTGCAGACCAAGAACTGGGTGATGCCCAT 120
QY 121 TCCTTGACCGGCTTCGCGAGACCAAGATCCCTAAAAGGAAGAGTAGCACTCTTGTC 180
DB 121 TCCTTGACCGGCTTCGCGAGACCAAGATCCCTAAAAGGAAGAGTAGCACTCTTGTC 180
QY 181 TGGACATCGAACAGCCACTCGTGGAGGAAGCAGATAGTGGAGCAGATTCTGGAGAGG 240
DB 181 TGGACATCGAACAGCCACTCGTGGAGGAAGCAGATAGTGGAGCAGATTCTGGAGAGG 240
QY 241 AATCAGATGAGGCACTTAAATGACCAATTTGCTGTCTCTGCTTCAAGCTTAACTG 300
DB 241 AATCAGATGAGGCACTTAAATGACCAATTTGCTGTCTCTGCTTCAAGCTTAACTG 300
QY 301 ACATGACTCTTGATGAGATGTCAAGAGACTGGTTCATGCTCATGCCCAAGCAGAAAGTAA 360
DB 301 ACATGACTCTTGATGAGATGTCAAGAGACTGGTTCATGCTCATGCCCAAGCAGAAAGTAA 360
QY 361 CAGGCTCCCTATGATTAAGATGACAGGCAATCATGGAATAGACATCATCTTAAAG 420
DB 361 CAGGCTCCCTATGATTAAGATGACAGGCAATCATGGAATAGACATCATCTTAAAG 420
QY 421 CAAACTTTAGTGTGATTTTGGAGGCTGGAGACCACTAATCTACTAGAGCTTACCG 480
DB 421 CAAACTTTAGTGTGATTTTGGAGGCTGGAGACCACTAATCTACTAGAGCTTACCG 480
QY 481 AAGAGAGAGCTGTGGGCAAAATTTCCATTTGCTCTCTTCCAGACATCTAATG 540
DB 481 AAGAGAGAGCTGTGGGCAAAATTTCCATTTGCTCTCTTCCAGACATCTAATG 540
QY 541 AGGATGTCAAAATGCAATTTGGGCTCTCATCGGAGGACTTAAATGGAATGAATACGG 600
DB 541 AGGATGTCAAAATGCAATTTGGGCTCTCATCGGAGGACTTAAATGGAATGAATACGG 600
QY 601 TTAGATCTCTGAAACTCTACAGAGATTCGCTTGGAGAGCAGTCAATGGAATGGAGAC 660
DB 601 TTAGATCTCTGAAACTCTACAGAGATTCGCTTGGAGAGCAGTCAATGGAATGGAGAC 660
QY 661 CTTCACTCCCTCCAAAGCAGACGAAATGGAGAGCAATTTGGAGCAGCTTGA 720
DB 661 CTTCACTCCCTCCAAAGCAGACGAAATGGAGAGCAATTTGGAGCAGCTTGA 720
QY 721 GAAATGAAGTGTGATTTGAAGAGTGGACATGATGAAATGAAATGCAAAATAGTTTT 780
DB 721 GAAATGAAGTGTGATTTGAAGAGTGGACATGATGAAATGAAATGCAAAATAGTTTT 780
QY 781 GAACTAAATCACTTTATGCAAGCTTTACACTATTTGCTTGAAGTGAACAGAGATAAGA 840
DB 781 GAACTAAATCACTTTATGCAAGCTTTACACTATTTGCTTGAAGTGAACAGAGATAAGA 840
QY 841 ACTTTCTGTTTCAAGCTTTATTAATGATAAAACACCCCTTGTCTTA 888
DB 841 ACTTTCTGTTTCAAGCTTTATTAATGATAAAACACCCCTTGTCTTA 888

RESULT 7
US-10-065-133A-53
; Sequence 53, Application US/10065133A

Publication No. US20030199074A1
GENERAL INFORMATION: Patricia W.
APPLICANT: Dowling, Patricia W.
APPLICANT: Younger, Julius S.
TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
FILE REFERENCE: EQ-1-C2-1
CURRENT APPLICATION NUMBER: US/10/065,133A
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: PCT/US99/18583
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 09/133,921
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn version 3.1
SEQ ID NO 53
LENGTH: 888
TYPE: DNA
ORGANISM: Equine influenza virus H3N8
US-10-065-133A-53

Query Match 99.6%; Score 884.4; DB 6; Length 888;
Best Local Similarity 99.9%; Pred. No. 3.2e-231;
Matches 885; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CAAAGCAGGGTGACAAAACATAATGGATTCCACACTGTGTCAAGCTTTTCAGTAGAC 62
DB 1 CAAAGCAGGGTGACAAAACATAATGGATTCCACACTGTGTCAAGCTTTTCAGTAGAC 60
QY 63 TGTGTTTCTTTGGCATGTCCGCAACGATTTGCAGACCAAGAACTGGGTGATGCCCATTC 122
DB 61 TGTGTTTCTTTGGCATGTCCGCAACGATTTGCAGACCAAGAACTGGGTGATGCCCATTC 120
QY 123 CTTGACCGGCTTCGCGAGACCAAGAGTCCCTAAAAGGAAGAGTAGCACTCTTGCTG 182
DB 121 CTTGACCGGCTTCGCGAGACCAAGAGTCCCTAAAAGGAAGAGTAGCACTCTTGCTG 180
QY 183 GACATCGAAACAGCACTTCGCGAGGAAGAGATAGTGGAGCAGATTCTGGAAGAGAA 242
DB 181 GACATCGAAACAGCACTTCGCGAGGAAGAGATAGTGGAGCAGATTCTGGAAGAGAA 240
QY 243 TCAGATGAGGCACTTAAATGACCAATTTGCTCTGTTCTGCTTCAAGCTTAACTGAC 302
DB 241 TCAGATGAGGCACTTAAATGACCAATTTGCTCTGTTCTGCTTCAAGCTTAACTGAC 300
QY 303 ATGACTCTTTGATGAGATGTCAAGAGACTGGTTTCATGCTCATGCCCAAGCAGAAAGTAA 362
DB 301 ATGACTCTTTGATGAGATGTCAAGAGACTGGTTTCATGCTCATGCCCAAGCAGAAAGTAA 360
QY 363 GGCTCCCTATGTATAAGAAATGGACCAATCATGATTAAGAAACATCATCTTAAAGCA 422
DB 361 GGCTCCCTATGTATAGAAATGGACCAATCATGATTAAGAAACATCATCTTAAAGCA 420
QY 423 AACTTTAGTGTGATTTTGGAGGCTGGAGCACTTAATCTATTAGAGCTTTCAAGCA 482
DB 421 AACTTTAGTGTGATTTTGGAGGCTGGAGCACTTAATCTATTAGAGCTTTCAAGCA 480
QY 483 GAAGGAGAGTGTGGGCAAAATTTCACTGCTTCTTCTTCCAGGACATCTAATGAG 542
DB 481 GAAGGAGAGTGTGGGCAAAATTTCACTGCTTCTTCTTCCAGGACATCTAATGAG 540
QY 543 GATGTCGAAATGCAATTTGGGCTCTCATCGGAGGACTTAAATGGAATGATTAATCGGTT 602
DB 541 GATGTCGAAATGCAATTTGGGCTCTCATCGGAGGACTTAAATGGAATGATTAATCGGTT 600
QY 603 AGAATCTCTGAACTCTACAGAGATTCGCTTGGAGAGCAGTCAATGGAATGGAAGCT 662
DB 601 AGAATCTCTGAACTCTACAGAGATTCGCTTGGAGAGCAGTCAATGGAATGGAAGCT 660
QY 663 TCATTCCCTCCAAAGCAGAAACGAAATGGAGAGCAATTTGAGCAGAGCTTTGAAGA 722
DB 661 TCATTCCCTCCAAAGCAGAAACGAAATGGAGAGCAATTTGAGCAGAGCTTTGAAGA 720
QY 723 AATAAGATGGTTGATTGGAAGAGTGGCAGCATAGATTGGAATAATAGATTTTGA 782

Db 721 AATAAGATGGTGTGATGATGAGAGTGGCGACATAGATTGAAATATACAGAAATAGTTTGA 780
Qy 783 ACAATATACATTATGCGAGCCTTACACTATTGCTTGAAGTAGAACAGAGATAAGAAC 842
Db 781 ACAATATACATTATGCGAGCCTTACACTATTGCTTGAAGTAGAACAGAGATAAGAAC 840
Qy 843 TTTCTCGTTTCAGCTTATTTAATGATATAAAGACACCTGTGTTCTA 888
Db 841 TTTCTCGTTTCAGCTTATTTAATGATATAAAGACACCTGTGTTCTA 886

RESULT 8
US-10-734-373-53
; Sequence 53, Application US/10734373
; Publication No. US20040137015A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/734,373
; PRIOR FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-734-373-53

Query Match 99.6%; Score 884.4; DB 7; Length 888;
Best Local Similarity 99.9%; Pred. No. 3.2e-231;
Matches 885; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CAAAGCAGGGTGACAAAAACATAATGATTCACACTGTGTCAAGCTTTAGGTAGAC 62
Db 1 CAAAGCAGGGTGACAAAAACATAATGATTCACACTGTGTCAAGCTTTAGGTAGAC 60
Qy 63 TGTGTTCTTTGGCATGTCCGCAACGATTTGCGAGCAAGAACTGGGTGATGCCCATTC 122
Db 61 TGTGTTCTTTGGCATGTCCGCAACGATTTGCGAGCAAGAACTGGGTGATGCCCATTC 120
Qy 123 CTTGACCGGCTTCGCGAGACCAAGTCCCTTAAAGGAGAGAGGTAGACACTCTTGTCTG 182
Db 121 CTTGACCGGCTTCGCGAGACCAAGTCCCTTAAAGGAGAGAGGTAGACACTCTTGTCTG 180
Qy 183 GACATCGAAACAGCCACTCGTGCAGAAAGCAGATAGTGGAGCAGATTCTGGAAGAGAA 242
Db 181 GACATCGAAACAGCCACTCGTGCAGAAAGCAGATAGTGGAGCAGATTCTGGAAGAGAA 240
Qy 243 TCAGATGAGGCACCTTAAATGACCAATGCTTCTGTTCCCTGCTTCAAGTACTTAACTGAC 302
Db 241 TCAGATGAGGCACCTTAAATGACCAATGCTTCTGTTCCCTGCTTCAAGTACTTAACTGAC 300
Qy 303 ATGACTCTTGATGAGATGTCAAGAGACTGGTTCAATGCTCATGCCCAAGCAGAAAGTAAAC 362
Db 301 ATGACTCTTGATGAGATGTCAAGAGACTGGTTCAATGCTCATGCCCAAGCAGAAAGTAAAC 360
Qy 363 GGTCTCCTATGATAAGATGGAACAGGCAATCATGGAAGAAACATCATATCTTAAAGCA 422
Db 361 GGTCTCCTATGATAAGATGGAACAGGCAATCATGGAAGAAACATCATATCTTAAAGCA 420
Qy 423 AACTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATATCTTAGAGCCCTTCAACGAA 482
Db 421 AACTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATATCTTAGAGCCCTTCAACGAA 480
Qy 483 GAAGGAGCAGTGGTGGCGAAATTTCCACATTTGCTTCTTCCAGGACATCAATATGAG 542

Db 481 GAAGGAGCAGTGGTGGCGAAATTTCCACATTTGCCTTCTCTCCAGGACATCAATATGAG 540
Qy 543 GATGTCAAAAATGCAATTTGGGTCTCTATCGAGGACTTAAATGCAATGATAATACGGTT 602
Db 541 GATGTCAAAAATGCAATTTGGGTCTCTATCGAGGACTTAAATGCAATGATAATACGGTT 600
Qy 603 AGAATCTCTGAAACTCTACAGAGATTCGTTGGAGAGCAGTCATGAGAAATGGGAGACCT 662
Db 601 AGAATCTCTGAAACTCTACAGAGATTCGTTGGAGAGCAGTCATGAGAAATGGGAGACCT 660
Qy 663 TCATTTCCCTCCAAAAGCAGAAACGAAAAATGAGAGAAACAATGAGCAGAGTTTGAGA 722
Db 661 TCATTTCCCTCCAAAAGCAGAAACGAAAAATGAGAGAAACAATGAGCAGAGTTTGAGA 720
Qy 723 AATAAGATGGTGTGATTCAGAGAGTGGACATAGATTGAAAAATACAGAAATAGTTTGA 782
Db 721 AATAAGATGGTGTGATTCAGAGAGTGGACATAGATTGAAAAATACAGAAATAGTTTGA 780
Qy 783 ACAATATACATTATGCAAGCCTTACACTATTGCTTGAAGTAGAACAGAGATAAGAAC 842
Db 781 ACAATATACATTATGCAAGCCTTACACTATTGCTTGAAGTAGAACAGAGATAAGAAC 840
Qy 843 TTTCTCGTTTCAGCTTATTTAATGATATAAAGACACCTGTGTTCTA 888
Db 841 TTTCTCGTTTCAGCTTATTTAATGATATAAAGACACCTGTGTTCTA 886

RESULT 9
US-10-181-585B-35
; Sequence 35, Application US/10181585B
; Publication No. US20050175985A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C3-PUS
; CURRENT APPLICATION NUMBER: US/10/181,585B
; CURRENT FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: PCT/US01/05048
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/506,286
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-181-585B-35

Query Match 99.6%; Score 884.4; DB 9; Length 888;
Best Local Similarity 99.9%; Pred. No. 3.2e-231;
Matches 885; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CAAAGCAGGGTGACAAAAACATAATGATTCACAACTGTGTCAAGCTTTAGGTAGAC 62
Db 1 CAAAGCAGGGTGACAAAAACATAATGATTCACAACTGTGTCAAGCTTTAGGTAGAC 60
Qy 63 TGTGTTCTTTGGCATGTCCGCAACGATTTGCGAGCAAGAACTGGGTGATGCCCATTC 122
Db 61 TGTGTTCTTTGGCATGTCCGCAACGATTTGCGAGCAAGAACTGGGTGATGCCCATTC 120
Qy 123 CTTGACCGGCTTCGCGAGACCAAGTCCCTTAAAGGAGAGAGGTAGACACTCTTGTCTG 182
Db 121 CTTGACCGGCTTCGCGAGACCAAGTCCCTTAAAGGAGAGAGGTAGACACTCTTGTCTG 180
Qy 183 GACATCGAAACAGCCACTCGTGCAGAAAGCAGATAGTGGAGCAGATTCTGGAAGAGAA 242
Db 181 GACATCGAAACAGCCACTCGTGCAGAAAGCAGATAGTGGAGCAGATTCTGGAAGAGAA 240
Qy 243 TCAGATGAGGCACCTTAAATGACCAATGCTTCTGTTCCCTGCTTCAAGTACTTAACTGAC 302

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Db 241 TCAGATGAGGACATTAATAATGACCATTCCTGCTGCTTCAAGCTACTTAACATGAC 300
Qy 303 ATGACTCTTGATGAGATGTCAAGAGACTGGTTTCATGCTCATGCTCCCAAGCAGAAAGTAACA 362
Db 301 ATGACTCTTGATGAGATGTCAAGAGACTGGTTTCATGCTCATGCTCCCAAGCAGAAAGTAACA 360
Qy 363 GGCTCCCTATGTATAAGAAATGGACAGGCAATCATGATAAGAAACATCATCTATAAGCA 422
Db 361 GGCTCCCTATGTATAAGAAATGGACAGGCAATCATGATAAGAAACATCATCTATAAGCA 420
Qy 423 AACTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATACTACTTAGAGCCTTCAACGAA 482
Db 421 AACTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATACTACTTAGAGCCTTCAACGAA 480
Qy 483 GAAGGAGCAGTGGTGGGAAATTCACCATTCGCTTCTTCCAGGACATCAATAGAG 542
Db 481 GAAGGAGCAGTGGTGGGAAATTCACCATTCGCTTCTTCCAGGACATCAATAGAG 540
Qy 543 GATGCTCAAAATGCATGGGGTCTCATCGAGAGCTTAAATGGAAATGATACGGTT 602
Db 541 GATGCTCAAAATGCATGGGGTCTCATCGAGAGCTTAAATGGAAATGATACGGTT 600
Qy 603 AGAATCTGAAACTCTACAGAGATTCGCTTGGAGAAAGCAGTCAAGAGATGGAGACCT 662
Db 601 AGAATCTGAAACTCTACAGAGATTCGCTTGGAGAAAGCAGTCAAGAGATGGAGACCT 660
Qy 663 TCATTCCCTCCAAAGCAGAAACGAAATGGAGAGAAATTCGAGCCAGAGTTTGAAGA 722
Db 661 TCATTCCCTCCAAAGCAGAAACGAAATGGAGAGAAATTCGAGCCAGAGTTTGAAGA 720
Qy 723 AATAAGATGGTTGATTCGAAAGTGGCAGATAGATTCGAAATACAGAAATAGTTTGA 782
Db 721 AATAAGATGGTTGATTCGAAAGTGGCAGATAGATTCGAAATACAGAAATAGTTTGA 780
Qy 783 ACAATAACATTTATGCAAGCCTTACAACTATTCGTTGAAGTAGACAGAGATAAGAC 842
Db 781 ACAATAACATTTATGCAAGCCTTACAACTATTCGTTGAAGTAGACAGAGATAAGAC 840
Qy 843 TTTCCTGTTTCACTTATTAATGATAAAGACCCCTGTTCTTA 888
Db 841 TTTCCTGTTTCACTTATTAATGATAAAGACCCCTGTTCTTA 886
```

RESULT 10

US-10-855-875-6

; Sequence 6, Application US/10855875

; Publication No. US2005000349A1

; GENERAL INFORMATION:

; APPLICANT: Kawaoka, Yoshihiro

; TITLE OF INVENTION: High Titer Recombinant Influenza Viruses for Vaccines and Gene Th

; FILE REFERENCE: 800.038U81

; CURRENT APPLICATION NUMBER: US/10/855,875

; CURRENT FILING DATE: 2004-05-27

; PRIOR APPLICATION NUMBER: US 60/473,798

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 890

; TYPE: DNA

; ORGANISM: Influenza virus

US-10-855-875-6

Query Match 83.6%; Score 742.4; DB 8; Length 890;

Best Local Similarity 89.8%; Pred. No. 2.4e-182;

Matches 797; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

Qy 1 AGCAAAAGCAGGTCACAAAACATTAATGGATTCACACTGTGTCAAGCTTTCAGTAG 60

Db 1 AGCAAAAGCAGGTCACAAAACATTAATGGATTCACACTGTGTCAAGCTTTCAGTAG 60

Qy 61 ACTGTTTCTTTGGCATGCTCCGCAAAACGATTTGGCAGACCAAGAACTGGGTGATGCCCAT 120

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Db 61 ATTGCTTCTTTGGCATGCTCCGCAAAACGATTTGCAGACCAAGAACTAGCGATGCCCAT 120
Qy 121 TCCTTCAACCGGCTTCGCGAGACCCAGAAAGTCCCTTAAAAAGGAAGAGGTAGCACTCTTGTGTC 180
Db 121 TCCTTCAACCGGCTTCGCGAGATCCCTTAAAGAGGAAGGGGAGTACTCTCGGTTC 180
Qy 181 TGGACATCAAAACGCCACTCGTGCAGGAAGACATAGTGGAGCAGATTTCTGGAGAGG 240
Db 181 TGGACATCAAGACACCCACAGCTGCTGGAAGACAGATAGTGGAGCGATTTCTGAAGAAG 240
Qy 241 AATCAGATCAGAGCATTAAATGATGACCATTCCTGCTGCTTCCCTTCAAGCTTAACTG 300
Db 241 AATCCGATGAGGCATTTAAATGATGACCATTCCTGCTGCTTCCCTTCAAGCTTAACTG 300
Qy 301 ACATGACTCTTCATGAGATGTCAAGAGACTGGTTTCATGCTCATGCTCCCAAGCAGAAAGTAA 360
Db 301 ACATGACTCTTCATGAGAAATGTCAAGGAGTGGTTCATGCTCATGCTCCCAAGCAGAAAGTGG 360
Qy 361 CAGGCTCCCTATGTATAAGAAATGGACAGGCAATCATGGAATAGAACATCATCTATAAG 420
Db 361 CAGGCTCCCTATGTATAAGAAATGGACAGGCAATCATGGAATAGAACATCATCTATAAG 420
Qy 421 CAACTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATACTACTTAGAGCCTTCAAGC 480
Db 421 CAACTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATACTACTTAGAGCCTTCAAGC 480
Qy 481 AAGAAGGAGCAGTCTGCTGGGAAATTTCAACCTTCCCTTCTTCCAGGACATCAATAAG 540
Db 481 AAGAAGGAGCAATTTCTGGGAAATTTCAACCTTCCCTTCTTCCAGGACATCAATAAG 540
Qy 541 AGGATCTCAAAATGCAATTTGGGCTCTCATCGAGGAGCTTAAATGGAATGATAATACGG 600
Db 541 AGGATCTCAAAATGCAATTTGGGCTCTCATCGAGGAGCTTGAATGGAATGATAATACAG 600
Qy 601 TTAGAACTCTCAAACTCTACAGAGATTCGCTTGGAGAGCAGTCAATGAGAAATGGAGAC 660
Db 601 TTGAGTCTCTGAAACTCTACAGAGATTCGCTTGGAGAGCAGTCAATGAGAAATGGAGAC 660
Qy 661 CTTTCATCTCCCAAGCAGAAAGCAAAATGGAGAGCAATTTGAGCCAGAGTTTGAAGA 720
Db 661 CTTTCATCTCCCAAGCAGAAAGCAAAATGGAGAGCAATTTGAGCCAGAGTTTGAAGA 720
Qy 721 GAAATAGATGTTGATTTGAGAGAGTGGCAGATAGATTTGAAATACAGAAATAGTTTT 780
Db 721 GAAATAGATGTTGATTTGAGAGAGTGGCAGATAGATTTGAAATACAGAAATAGTTTT 780
Qy 781 GAACAAAATACATTTATGCAAGCCTTACAACTATTTGCTTGAAGTAGAACAAGAGATAAGA 840
Db 781 GAGCAAAATACATTTATGCAAGCCTTACATCTATTTGCTTGAAGTAGGAGCAAGAGATAAGA 840
Qy 841 ACTTTCCTGTTTCACTTATTAATGATAAAGCAACCCCTGTTTCTTA 888
Db 841 ACTTTCCTGTTTCACTTATTAATGATAAAGCAACCCCTGTTTCTTA 888
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RESULT 11

US-10-381-530-8

; Sequence 8, Application US/10381530

; Publication No. US20040137013A1

; GENERAL INFORMATION:

; APPLICANT: KATINGER, Hermann

; APPLICANT: EGOROV, Andre

; APPLICANT: FERKO, Boris

; APPLICANT: ROMANOVA, Julia

; APPLICANT: KATINGER, Dietmar

; TITLE OF INVENTION: LIVE VACCINE AND METHOD OF MANUFACTURE

; FILE REFERENCE: P/167-134

; CURRENT APPLICATION NUMBER: US/10/381,530

; CURRENT FILING DATE: 2003-11-24

; PRIOR APPLICATION NUMBER: PCT/EP01/11087

; PRIOR FILING DATE: 2001-09-25

; PRIOR APPLICATION NUMBER: 00120896.6

RESULT 12
US-10-654-737-2
; Sequence 2, Application US/10654737
; Publication No. US20050054846A1
; GENERAL INFORMATION:
; APPLICANT: St. Jude Children's Research Hospital
; APPLICANT: Webster, Robert G
; APPLICANT: Webby, Richard J
; APPLICANT: Ozaki, Hirochi
; TITLE OF INVENTION: Improved Method for Generating Influenza Viruses and Vaccines
; FILE REFERENCE: SJ-02-0016
; CURRENT APPLICATION NUMBER: US/10/654,737
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 824
; TYPE: DNA
; ORGANISM: Influenza A virus
US-10-654-737-2

Query Match 78.0%; Score 692.8; DB 9; Length 824;
Best Local Similarity 90.0%; Pred. No. 8.6e-179;
Matches 742; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 22 ACATAATGGATTCCCAACACCTGTGTCAAGCTTTTCAGGTAGACTGTTTTCTTTGGCATGTCC 81
DB 1 ACATAATGGATTCCCAACACCTGTGTCAAGCTTTTCAGGTAGACTGTTTTCTTTGGCATGTCC 60
QY 82 GCAAACGATTTTCAGACCAAGAACTGGGTGATGCCCCCAITTCCTTGACCGGCTTCGCCGAG 141
DB 61 GCAAACGATTTTCAGACCAAGAACTGGGTGATGCCCCCAITTCCTTGATCGGCTTCGCCGAG 120
QY 142 ACCGAGATTCCTTAAGAGGAAGAGGTAGCACTCTTGTCTTGACATCGAAACACGCCACTC 201
DB 121 ATCGAAGTTCCTTAAGAGGAAGAGGCAGCACTCTCGGCTCGAACAACGAAACGCCACTC 180
QY 202 GTCAGCAAGCAAGCATATGTCGACGATTTCTGGAAGAGGAATCAGATGAGGCACCTTAAAA 261
DB 181 GTCTGCAAGCAAGCATATGTCGACGATTTCTGGAAGAGGAATCCGATGAGGCACCTTAAAA 240
QY 262 TGACCATTCCTCTGTTCTGCTTCACTGCTTCACTTAATGATGATGATGATGATGATGATGATG 321
DB 241 TGACCATTCCTCTGCTTCACTGCTTCACTTAATGATGATGATGATGATGATGATGATGATG 300
QY 322 CAGAGATGCTGTTCACTGCTCATCGCCCAAGCAAGAAAGTAAAGCGCTCCCTATGATATAGAA 381
DB 301 CAGAGATGCTGTTCACTGCTCATCGCCCAAGCAAGAAAGTAAAGCGCTCCCTATGATATAGAA 360
QY 382 TGGACACGCGCAATCATGATAGCAATCATATCTTTTAAGCAAACTTTAGTGTGATTTTCG 441
DB 361 TGGACACGCGCAATCATGATAGCAATCATATCTTTTAAGCAAACTTTAGTGTGATTTTCG 420
QY 442 AAAGGCTTGGAGACATTAATCTACTTCTAGAGCTTCACCGAGAGGAGGAGGAGGAGGAGGAG 501
DB 421 ACCGGCTTGGAGACATTAATCTACTTCTAGAGCTTCACCGAGAGGAGGAGGAGGAGGAGGAG 480
QY 502 AAATTTTCACTATGCTTCTCTTCAGGACATCTAATGAGGATGTCMAAATGCAATTTG 561
DB 481 AAATTTTCACTATGCTTCTCTTCAGGACATCTAATGAGGATGTCMAAATGCAATTTG 540
QY 562 GGGTCTCTCATCGGAGGACTTAATGGAATGATATACCGTTAGAACTCTCTGAACTCTTAC 621
DB 541 GGGTCTCTCATCGGAGGACTTAATGGAATGATATACCGTTAGAACTCTCTGAACTCTTAC 600
QY 622 AGAGATTGCTTTCGAGAAAGCAGTCAATGAGAAATGGGAGACTTCTTCTTCTTCTTCTTCTT 681
DB 601 AGAGATTGCTTTCGAGAAAGCAGTCAATGAGAAATGGGAGACTTCTTCTTCTTCTTCTTCTT 660
QY 682 AACGAAAAATGGAGAGAAACAAATTGAGCCAGAACTTTTGAAGAAATAAGATGTTGATGAA 741
DB 661 AACGAAAAATGGAGAGAAACAAATTGAGCCAGAACTTTTGAAGAAATAAGATGTTGATGAA 720

PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 890
; TYPE: DNA
; ORGANISM: Influenza virus A/Singapore/1/57/ca
US-10-381-530-8

Query Match 83.1%; Score 737.6; DB 7; Length 890;
Best Local Similarity 89.4%; Pred. No. 4.9e-191;
Matches 794; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 1 AGCAAAAGCAGGGTGACAAAACATATATGGATTCACACACTGTGTCAAGCTTTTCAGGTAG 60
DB 1 AGCAAAAGCAGGGTGACAAAACATATATGGATTCACACACTGTGTGTCAAGCTTTTCAGGTAG 60
QY 61 ACTGTTTTCTTTGGCATGTTCGCAACAGTATTCGACCCAGAACTGGGTGATGCCCCAT 120
DB 61 ATTGCTTCTTTGGCATGTTCGCAACAGTATTCGACCCAGAACTGGGTGATGCCCCAT 120
QY 121 TCCTTGACCGGCTTCGCCGAGACACGAAGTCCCTTAAAGGAGAGAGGTAGCACTCTTGCTC 180
DB 121 TCCTTGATCGGCTTCGCCGAGATTCGAAGTCCCTTAAAGGAGAGAGGTAGCACTCTTGCTC 180
QY 181 TGAACATCGAAACAGCCACTCGTCGAGGAAGACGATAGTGGAGCAGATTCGAGAGAG 240
DB 181 TGAACATCGAAACAGCCACTCGTCGAGGAAGACGATAGTGGAGAGAGATTCGAGAGAG 240
QY 241 AATCAGATGAGGCACTTAAATGACCATGCGCTGCTGCTCTGCTCAGCTACTTAATCTG 300
DB 241 AATCAGATGAGGCACTTAAATGACCATGCGCTGCTGCTCAGCTACTTAATCTG 300
QY 301 ACATGACTCTTGATGAGATGTCAAGAGACTGGTTCATGCTCATGCCCAGCAGAAAGTAA 360
DB 301 ACATGACTCTTGATGAGATGTCAAGAGACTGGTTCATGCTCATGCCCAGCAGAAAGTGT 360
QY 361 CAGGCTCCCTATGTATAGAAATGACACAGGCAATCATGATATAGAAACATCATACTTAAG 420
DB 361 CAGGCTCCCTATGTATAGAAATGACACAGGCAATCATGATATAGAAACATCATACTTAAG 420
QY 421 CAAACTTTAGTGTGATTTTTCGAAAGGCTGGAGACATAATACTACTTAGAGCCTTCAACG 480
DB 421 CAAACTTTAGTGTGATTTTTCGAAAGGCTGGAGACATAATACTACTTAGAGCCTTCAACG 480
QY 481 AAGAGGAGCAGTCTGTGCGCAAAATTTCAACATTCGCTTCTCTTCAGGACATACATATG 540
DB 481 AAGAGGAGCAGTCTGTGCGCAAAATTTCAACATTCGCTTCTCTTCAGGACATACATATG 540
QY 541 AGGATGTCAAAATGCAATTTGGGCTCTCATCGAGGACTTAAATGGAATGATAATACGG 600
DB 541 AGGATGTCAAAATGCAATTTGGGCTCTCATCGAGGACTTAAATGGAATGATAATACGG 600
QY 601 TTGAATCTCTGAACTCTACAGAGATTCCTTTGGAGAGCAGTATGAGATGGAGAG 660
DB 601 TTGAGTCTCTAATCTCTACAGAGATTCCTTTGGAGAGCAGTATGAGATGGAGAG 660
QY 661 CTTCCTCTCTTCAAAACGAAACGGAATTTGGAGAGCAATTTGAGCAAGTTCGAA 720
DB 661 CTTCCTCTCTTCAAAACGGAATTTGGAGAGCAATTTGAGCAAGTTCGAA 720
QY 721 GAATATGAGTGTGATTCGAGAGTGGGACATAGATTCGAAATGCAAAATAGTATTT 780
DB 721 GAATATGAGTGTGATTCGAGAGTGGGACATAGATTCGAAATGCAAAATAGTATTT 780
QY 781 GAACAAATATCATTTATGACCTTACACTATCTGCTTGAAGTGAACAGAGATTAAGA 840
DB 781 GAGCAAAATACATTTATGACGCTTACACTATCTGCTTGAAGTGAACAGAGATTAAGA 840
QY 841 ACTTTCTCGTTTACGCTTATTTAATGATTAATAAACCCTTCTTCTA 888
DB 841 ACTTTCTCGTTTACGCTTATTTAATGATTAATAAACCCTTCTTCTA 888

Qy 742 GAAATGCGACATAGATTGAAATAACAGAAATAGTTTGAACAAATACATTTATGCAA 801
Db 721 GAAATGCGACATAGATTGAAATAACAGAAATAGTTTGAACAAATACATTTATGCAA 780
Qy 802 GCGTTTACCACTATTGCTTGAAGTAGAACAAGAGATAAGAACTTT 845
Db 781 GCGTTTACCACTATTGCTTGAAGTAGAACAAGAGATAAGAACTTT 824

RESULT 13

US-10-065-133A-52
; Sequence 52, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 52
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-52

Query Match 77.7%; Score 690; DB 6; Length 690;
Best Local Similarity 100.0%; Pred. No. 4.6e-178;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ATGATTTCCAACTGTCAGCTTTTCAGTGTAGCTGTTTCTTTGGCATGTCGCCAAA 86
Db 1 ATGATTTCCAACTGTCAGCTTTTCAGTGTAGCTGTTTCTTTGGCATGTCGCCAAA 60
Qy 87 CGATTTCCAGACCAAGAACTGGGTGATGCCCCATTCCTGACCGGCTTCGCCGAGACG 146
Db 61 CGATTTCCAGACCAAGAACTGGGTGATGCCCCATTCCTGACCGGCTTCGCCGAGACG 120
Qy 147 AAGTCCCTTAAAGAGAGGTAGCACTCTTGGTCTGGACATCGAAGACGCACTCGTGA 206
Db 121 AAGTCCCTTAAAGAGAGGTAGCACTCTTGGTCTGGACATCGAAGACGCACTCGTGA 180
Qy 207 GGAAGCAGATAGTGAGCAGATTCTGGAAGAGGAATCAGATGAGGCACTTAAATGACC 266
Db 181 GGAAGCAGATAGTGAGCAGATTCTGGAAGAGGAATCAGATGAGGCACTTAAATGACC 240
Qy 267 ATTGCCTCTGTTCTCTGCTTCAAGCAGATGATGAGGCACTTAAATGACC 326
Db 241 ATTGCCTCTGTTCTCTGCTTCAAGCAGATGATGAGGCACTTAAATGACC 300
Qy 327 GACTGGTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTATGTATGAAGATGGAC 386
Db 301 GACTGGTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTATGTATGAAGATGGAC 360
Qy 387 CAGCAATCATGATAGAAATCATATCTTAAAGCAAACTTTAGTGTGATTTTGAAGG 446
Db 361 CAGCAATCATGATAGAAATCATATCTTAAAGCAAACTTTAGTGTGATTTTGAAGG 420
Qy 447 CTGGAGCACTATATCTTAAAGCAAACTTTAGTGTGATTTTGAAGG 506
Db 421 CTGGAGCACTATATCTTAAAGCAAACTTTAGTGTGATTTTGAAGG 480
Qy 507 TCACATTTGCTTCTCTTCCAGGACATCTAATAGAGATGTCAAAATGCAATTTGGGGTC 566
Db 481 TCACATTTGCTTCTCTTCCAGGACATCTAATAGAGATGTCAAAATGCAATTTGGGGTC 540

Qy 567 CTATCGGAGGACCTTAAATGGAATGATATACGGTTAGAACTCTTGAAACTCTACAGAGA 626
Db 541 CTATCGGAGGACCTTAAATGGAATGATATACGGTTAGAACTCTTGAAACTCTACAGAGA 600
Qy 627 TTGCTTTGAGAGAGCAGTCATGAGAAATGGAGACCTTCATTCCCTCCAAAGCAGAAACGA 686
Db 601 TTGCTTTGAGAGAGCAGTCATGAGAAATGGAGACCTTCATTCCCTCCAAAGCAGAAACGA 660
Qy 687 AAAATGGAGAGAACAAATTTGAGCCAGAAAGTT 716
Db 661 AAAATGGAGAGAACAAATTTGAGCCAGAAAGTT 690

RESULT 14

US-10-065-133A-59
; Sequence 59, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 59
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-59

Query Match 77.7%; Score 690; DB 6; Length 690;
Best Local Similarity 100.0%; Pred. No. 4.6e-178;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ATGATTTCCAACTGTCAGCTTTTCAGTGTAGCTGTTTCTTTGGCATGTCGCCAAA 86
Db 1 ATGATTTCCAACTGTCAGCTTTTCAGTGTAGCTGTTTCTTTGGCATGTCGCCAAA 60
Qy 87 CGATTTCCAGACCAAGAACTGGGTGATGCCCCATTCCTGACCGGCTTCGCCGAGACG 146
Db 61 CGATTTCCAGACCAAGAACTGGGTGATGCCCCATTCCTGACCGGCTTCGCCGAGACG 120
Qy 147 AAGTCCCTTAAAGAGAGGTAGCACTCTTGGTCTGGACATCGAAGACGCACTCGTGA 206
Db 121 AAGTCCCTTAAAGAGAGGTAGCACTCTTGGTCTGGACATCGAAGACGCACTCGTGA 180
Qy 207 GGAAGCAGATAGTGAGCAGATTCTGGAAGAGGAATCAGATGAGGCACTTAAATGACC 266
Db 181 GGAAGCAGATAGTGAGCAGATTCTGGAAGAGGAATCAGATGAGGCACTTAAATGACC 240
Qy 267 ATTGCCTCTGTTCTCTGCTTCAAGCAGATGATGAGGCACTTAAATGACC 326
Db 241 ATTGCCTCTGTTCTCTGCTTCAAGCAGATGATGAGGCACTTAAATGACC 300
Qy 327 GACTGGTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTATGTATGAAGATGGAC 386
Db 301 GACTGGTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTATGTATGAAGATGGAC 360
Qy 387 CAGCAATCATGATAGAAATCATATCTTAAAGCAAACTTTAGTGTGATTTTGAAGG 446
Db 361 CAGCAATCATGATAGAAATCATATCTTAAAGCAAACTTTAGTGTGATTTTGAAGG 420
Qy 447 CTGGAGCACTATATCTTAAAGCAAACTTTAGTGTGATTTTGAAGG 506
Db 421 CTGGAGCACTATATCTTAAAGCAAACTTTAGTGTGATTTTGAAGG 480
Qy 507 TCACATTTGCTTCTCTTCCAGGACATCTAATAGAGATGTCAAAATGCAATTTGGGGTC 566

Db 481 TCACCAATGCCTTCTCTCCAGGACATATAATGAGGATGTCAAAAATGCAATTGGGGTC 540
Qy 567 CTCATCGGAGGACTTAAATGGAATGATATACGGTTAGAACTCTCTGAAACTCTACAGAGA 626
Db 541 CTCATCGGAGGACTTAAATGGAATGATATACGGTTAGAACTCTCTGAAACTCTACAGAGA 600
Qy 627 TTCGCTTGGAGAGCAGTCATGAGATGGAGACCTTCATTCCCTCCAAAGCAGAAACGA 686
Db 601 TTCGCTTGGAGAGCAGTCATGAGATGGAGACCTTCATTCCCTCCAAAGCAGAAACGA 660
Qy 687 AAAATGGAGAGCAATTTGAGCCAGAGTT 716
Db 661 AAAATGGAGAGCAATTTGAGCCAGAGTT 690

RESULT 15
US-10-734-373-52
; Sequence 52, Application US/10734373
; Publication No. US20040137015A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/734,373
; PRIOR FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-734-373-52

Query Match 77.7%; Score 690; DB 7; Length 690;
Best Local Similarity 100.0%; Pred. No. 4.6e-178;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 27 ATGGATTCCAAACACTGTCTCAAGCTTTCAGGTAGACTGTCTTTCTTTGGCATGTCCGCAA 86
Db 1 ATGGATTCCAAACACTGTCTCAAGCTTTCAGGTAGACTGTCTTTCTTTGGCATGTCCGCAA 60
Qy 87 CGATTTTCAGACCAAGAACTGGGTGATGCCCATTCCTTTGACCGGCTTTCGCGAGACCA 146
Db 61 CGATTTTCAGACCAAGAACTGGGTGATGCCCATTCCTTTGACCGGCTTTCGCGAGACCA 120
Qy 147 AAGTCCCTAAAGAGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCACTCGTGCA 206
Db 121 AAGTCCCTAAAGAGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCACTCGTGCA 180
Qy 207 GGAAGCAGATAGTGAGCAGATTCGGAAGAGGAATCAGATGAGGCACTTAAATGACC 266
Db 181 GGAAGCAGATAGTGAGCAGATTCGGAAGAGGAATCAGATGAGGCACTTAAATGACC 240
Qy 267 ATTGCCTCTGTCTCTGCTTCAAGCTTAACTGACATGACTCTTTGATGAGATGTCAAGA 326
Db 241 ATTGCCTCTGTCTCTGCTTCAAGCTTAACTGACATGACTCTTTGATGAGATGTCAAGA 300
Qy 327 GACTGGTTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTATGTATAAGATGGAC 386
Db 301 GACTGGTTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTATGTATAAGATGGAC 360
Qy 387 CAGGCAATCATGATAGAAACATCATACTTTAAAGCAAACTTTAGTGTGATTTTCGAAAGG 446
Db 361 CAGGCAATCATGATAGAAACATCATACTTTAAAGCAAACTTTAGTGTGATTTTCGAAAGG 420
Qy 447 CTGGAGACACTAATACTACTTAGAGCCTTCACCGAAGAGGAGCAGTGTGTGGCGAAATT 506

Db 421 CTGGAGACACTAATACTACTTTAGAGCCTTCAACGGAAGAGGAGCACTGTGTGGCGAAATT 480
Qy 507 TCACCAATGCCTTCTCTTCAGGACATATAATGAGGATGTCAAAAATGCAATTGGGGTC 566
Db 481 TCACCAATGCCTTCTCTTCAGGACATATAATGAGGATGTCAAAAATGCAATTGGGGTC 540
Qy 567 CTCATCGGAGGACTTAAATGGAATGATATACGGTTAGAACTCTCTGAAACTCTACAGAGA 626
Db 541 CTCATCGGAGGACTTAAATGGAATGATATACGGTTAGAACTCTCTGAAACTCTACAGAGA 600
Qy 627 TTCGCTTGGAGAGCAGTCATGAGATGGAGACCTTCATTCCCTCCAAAGCAGAAACGA 686
Db 601 TTCGCTTGGAGAGCAGTCATGAGATGGAGACCTTCATTCCCTCCAAAGCAGAAACGA 660
Qy 687 AAAATGGAGAGCAATTTGAGCCAGAGTT 716
Db 661 AAAATGGAGAGCAATTTGAGCCAGAGTT 690

Search completed: March 8, 2006, 04:48:05
Job time : 927.202 secs

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OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 01:03:53 ; Search time 416.426 Seconds
(without alignments)
4675.326 Million cell updates/sec

Title: US-10-734-373-57

Perfect score: 888

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 14437070

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New:

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- 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
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- 10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	41.2	4.6	218821	12	US-11-121-086-31 Sequence 31, Appl
C 2	40.8	4.6	2295	8	US-10-750-185-31619 Sequence 31619, A
C 3	40.8	4.6	2295	8	US-10-750-623-31619 Sequence 31619, A
C 4	39.8	4.5	566	6	US-09-925-065A-553911 Sequence 553911, A
C 5	39.8	4.5	1524	6	US-09-925-065A-553280 Sequence 553280, A
C 6	39.2	4.4	626	6	US-09-925-065A-408866 Sequence 408866, A
C 7	39.2	4.4	1279	6	US-09-925-065A-92744 Sequence 92744, A
C 8	39.2	4.4	1279	6	US-09-925-065A-92745 Sequence 92745, A
C 9	39	4.4	584	6	US-09-925-065A-452283 Sequence 452283, A
C 10	38.8	4.4	483	6	US-09-925-065A-597659 Sequence 597659, A
C 11	38.8	4.4	528	6	US-09-925-065A-597659 Sequence 597659, A
C 12	38.4	4.3	549	6	US-09-925-065A-279044 Sequence 279044, A
C 13	38.4	4.3	549	6	US-09-925-065A-279045 Sequence 279045, A
C 14	38.4	4.3	623	6	US-09-925-065A-766520 Sequence 766520, A
C 15	38.4	4.3	631	6	US-09-925-065A-771317 Sequence 771317, A
C 16	38.2	4.3	575	6	US-09-925-065A-354936 Sequence 354936, A
C 17	38	4.3	581	6	US-09-925-065A-632446 Sequence 632446, A
C 18	38	4.3	2721	8	US-10-750-185-52450 Sequence 52450, A
C 19	38	4.3	2721	8	US-10-750-623-52450 Sequence 52450, A
C 20	37.8	4.3	474	6	US-09-925-065A-543248 Sequence 543248, A

C 21	37.8	4.3	617	6	US-09-925-065A-576543 Sequence 576543, A
C 22	37.8	4.3	700	6	US-09-925-065A-165231 Sequence 165231, A
C 23	37.6	4.2	537	6	US-09-925-065A-336212 Sequence 336212, A
C 24	37.6	4.2	537	6	US-09-925-065A-336213 Sequence 336213, A
C 25	37.6	4.2	682	5	US-09-925-065A-360A-120 Sequence 120, Appl
C 26	37.6	4.2	1263	8	US-10-527-500-14 Sequence 14, Appl
C 27	37.6	4.2	121160	7	US-10-330-773-847 Sequence 847, Appl
C 28	37.6	4.2	254396	7	US-10-330-773-534 Sequence 534, Appl
C 29	37.4	4.2	635	6	US-09-925-065A-515303 Sequence 515303, A
C 30	37.4	4.2	1084	6	US-09-925-065A-704356 Sequence 704356, A
C 31	37.4	4.2	3850	6	US-09-925-065A-690067 Sequence 690067, A
C 32	37.2	4.2	242	6	US-09-925-065A-410546 Sequence 410546, A
C 33	37.2	4.2	530	6	US-09-925-065A-357347 Sequence 357347, A
C 34	37.2	4.2	110469	7	US-10-330-773-314 Sequence 314, Appl
C 35	37	4.2	172649	12	US-11-121-086-36 Sequence 36, Appl
C 36	36.8	4.1	578	6	US-09-925-065A-82370 Sequence 82370, A
C 37	36.8	4.1	622	6	US-09-925-065A-758895 Sequence 758895, A
C 38	36.8	4.1	623	6	US-09-925-065A-749905 Sequence 749905, A
C 39	36.8	4.1	676	6	US-09-925-065A-524064 Sequence 524064, A
C 40	36.8	4.1	1564	8	US-10-750-185-52400 Sequence 52400, A
C 41	36.8	4.1	1564	8	US-10-750-623-52400 Sequence 52400, A
C 42	36.8	4.1	2131	6	US-09-925-065A-74502 Sequence 74502, A
C 43	36.8	4.1	2131	6	US-09-925-065A-74503 Sequence 74503, A
C 44	36.8	4.1	2131	6	US-09-925-065A-74504 Sequence 74504, A
C 45	36.8	4.1	2131	6	US-09-925-065A-74505 Sequence 74505, A

ALIGNMENTS

RESULT 1
US-11-121-086-31/c
; Sequence 31, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138 6000-00000
; CURRENT APPLICATION NUMBER: US/11121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31
; LENGTH: 218821
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (106949)..(106949)
; OTHER INFORMATION: a, c, g, t, unknown or other
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (110322)..(110324)
; OTHER INFORMATION: a, c, g, t, unknown or other
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (115133)..(115133)
; OTHER INFORMATION: a, c, g, t, unknown or other
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (131300)..(131300)
; OTHER INFORMATION: a, c, g, t, unknown or other
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (139059)..(139158)
; OTHER INFORMATION: a, c, g, t, unknown or other
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (157740)..(157740)
; OTHER INFORMATION: a, c, g, t, unknown or other

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LOCATION: (200349)..(200349)
OTHER INFORMATION: a, c, g, t, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (200351)..(200351)
OTHER INFORMATION: a, c, g, t, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (212425)..(212426)
OTHER INFORMATION: a, c, g, t, unknown or other
US-11-121-086-31

Query Match 4.6%; Score 41.2; DB 12; Length 218821;
Best Local Similarity 53.0%; Pred. No. 20;
Matches 88; Conservative 0; Mismatches 78; Indels 0; Gaps 0;
QY 657 AGACCTTCATCCCTCCAAAGCAGAAACGAAAGTGGAGAGACAAATGGCCGAGATT 716
DB 125425 AAAATACAAACCAATAAGTAAATAAGAAAGAGAAAGATTAATTCAGAAATT 125365
QY 717 TGAAGAAATAAGATGGTTGATTGAGAGAGTGGACATAGATTGAAAATACAGAAATAG 776
DB 125365 TGATGTTAAACATCTGTGATGAAGATGCCAAAACAAATGTTTAAAGGCATTAATAG 125306
QY 777 TTTTGAACAAATAACATTTATGCAAGCTTACACTATGCTTGA 822
DB 125305 CCTGGAGAGAGAAATTTCTGTAAGTATTCATAATATTTAGTGAA 125260

RESULT 2
US-10-750-185-31619
Sequence 31619, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-2
CURRENT APPLICATION NUMBER: US/10750,185
PRIOR FILING DATE: 2003-12-31
PRIOR FILING DATE: 2003-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31619
LENGTH: 2295
TYPE: DNA
ORGANISM: Bovine 19866881194314
US-10-750-185-31619

Query Match 4.6%; Score 40.8; DB 8; Length 2295;
Best Local Similarity 49.5%; Pred. No. 5;
Matches 105; Conservative 0; Mismatches 107; Indels 0; Gaps 0;
QY 662 TTCAATTCCTCCAAAGCAGAAACGAAATAATGGAGAGACAAATTCAGCCGAGAGTTTGAAG 721
DB 1191 TTCTTTCTCGAAGATTTGAAAGGTTAAGTGAATTCAGAAATTTGATACTATGTTTCATAA 1250
QY 722 AAATAAGATGGTTGATTGAAGAAGTCGACATAGATTGAAAATACAGAAATAGTTTGG 781
DB 1251 AAATTAAGAAATGAGAAATAATGTTTAACTGAACTAGAACATAGAAAGTAAAGCACTT 1310
QY 782 AACAAATAACATTTATGCAAGCTTACACTATGCTTGAAGTGAAGAGAGATAAGAA 841
DB 1311 CAAATATATACCTTAATGTCCTAACCACTTCAGTACTGTTTTCATACATTCAGAGTAT 1370
QY 842 CTTCCTCGTTTCAGCTTATTAATGATAAAA 873

DB 1371 CTCACCTTTTCTGTTGTTTATGCTCATAAA 1402
RESULT 3
US-10-750-623-31619
Sequence 31619, Application US/10750623
Publication No. US20050287531A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-1
CURRENT APPLICATION NUMBER: US/10750,623
PRIOR FILING DATE: 2003-12-31
PRIOR FILING DATE: 2003-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31619
LENGTH: 2295
TYPE: DNA
ORGANISM: Bovine 19866881194314
US-10-750-623-31619

Query Match 4.6%; Score 40.8; DB 8; Length 2295;
Best Local Similarity 49.5%; Pred. No. 5;
Matches 105; Conservative 0; Mismatches 107; Indels 0; Gaps 0;
QY 662 TTCAATTCCTCCAAAGCAGAAACGAAATAATGGAGAGACAAATTCAGCCGAGAGTTTGAAG 721
DB 1191 TTCTTTCTCGAAGATTTGAAAGGTTAAGTGAATTCAGAAATTTGATACTATGTTTCATAA 1250
QY 722 AAATAAGATGGTTGATTGAAGAAGTCGACATAGATTGAAAATACAGAAATAGTTTGG 781
DB 1251 AAATTAAGAAATGAGAAATAATGTTTAACTGAACTAGAACATAGAAAGTAAAGCACTT 1310
QY 782 AACAAATAACATTTATGCAAGCTTACACTATGCTTGAAGTGAAGAGAGATAAGAA 841
DB 1311 CAAATATATACCTTAATGTCCTAACCACTTCAGTACTGTTTTCATACATTCAGAGTAT 1370
QY 842 CTTCCTCGTTTCAGCTTATTAATGATAAAA 873
DB 1371 CTCACCTTTTCTGTTGTTTATGCTCATAAA 1402

RESULT 4
US-09-925-065A-553911
Sequence 553911, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR FILING DATE: 2001-08-08
PRIOR FILING DATE: 2001-08-08
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0

; PRIOR APPLICATION NUMBER: US 60/289,846
 ; PRIOR FILING DATE: 2001-05-09
 ; NUMBER OF SEQ ID NOS: 957086
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 92744
 ; LENGTH: 1279
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (1)...(1279)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-925-065A-92744

Query Match 4.4%; Score 39.2; DB 6; Length 1279;
 Best Local Similarity 49.1%; Pred. No. 10;
 Matches 104; Conservative 0; Mismatches 108; Indels 0; Gaps 0;
 QY 674 AAGCAGAAACGAAATGCGAGAGACAAATTTGAGCCAGAGCTTTCAACAATAAGATGTT 733
 DB 584 AGATGAT 643
 QY 734 TGATTGAGAGAGTGGCAGATAGATTGAAAAATACAGAAAAATAGTTTGAACAAATAACAT 793
 DB 644 TAAGAGAGAGTAAAT 703
 QY 794 TTATGCAAGCCTTACAACTATTGCTTGAAGTAGAAGAGAGATAGAACTTTCTCGTTTC 853
 DB 704 TTAAGAAAAAGAT 763
 QY 854 AGCTTATTTAATGAT 885
 DB 764 GCCCATCTCAGTCCATCTTTCAACCTATCTT 795

RESULT 8
 US-09-925-065A-92745
 ; Sequence 92745, Application US/09925065A
 ; Publication No. US20040181048A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single
 ; FILE REFERENCE: 108827.135
 ; CURRENT APPLICATION NUMBER: US/09/925,065A
 ; PRIOR FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: US 60/243,096
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: US 60/252,147
 ; PRIOR FILING DATE: 2000-11-20
 ; PRIOR APPLICATION NUMBER: US 60/250,092
 ; PRIOR FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: US 60/261,766
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/289,846
 ; NUMBER OF SEQ ID NOS: 957086
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 92745
 ; LENGTH: 1279
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (1)...(1279)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-925-065A-92745

Query Match 4.4%; Score 39.2; DB 6; Length 1279;
 Best Local Similarity 49.1%; Pred. No. 10;
 Matches 104; Conservative 0; Mismatches 108; Indels 0; Gaps 0;
 QY 674 AAGCAGAAACGAAATGCGAGAGACAAATTTGAGCCAGAGCTTTCAACAATAAGATGTT 733

DB 584 AGATGAT 643
 QY 734 TGATTGAGAGAGTGGCAGATAGATTGAAAAATACAGAAAAATAGTTTGAACAAATAACAT 793
 DB 644 TAAGAGAGAGTAAAT 703
 QY 794 TTATGCAAGCCTTACAACTATTGCTTGAAGTAGAAGAGAGATAGAACTTTCTCGTTTC 853
 DB 704 TTAAGAAAAAGAT 763
 QY 854 AGCTTATTTAATGAT 885
 DB 764 GCCCATCTCAGTCCATCTTTCAACCTATCTT 795

RESULT 9
 US-09-925-065A-452283/C
 ; Sequence 452283, Application US/09925065A
 ; Publication No. US20040181048A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single
 ; FILE REFERENCE: 108827.135
 ; CURRENT APPLICATION NUMBER: US/09/925,065A
 ; PRIOR FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: US 60/243,096
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: US 60/252,147
 ; PRIOR FILING DATE: 2000-11-20
 ; PRIOR APPLICATION NUMBER: US 60/250,092
 ; PRIOR FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: US 60/261,766
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/289,846
 ; NUMBER OF SEQ ID NOS: 957086
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 452283
 ; LENGTH: 584
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-925-065A-452283

Query Match 4.4%; Score 39; DB 6; Length 584;
 Best Local Similarity 50.8%; Pred. No. 8.4;
 Matches 90; Conservative 1; Mismatches 86; Indels 0; Gaps 0;
 QY 712 AAGTTTGAAGAAATAAGATGTTGATTGAAGAGTGGCAGATAGATTGAAAAATACAGAA 771
 DB 233 AACAGTAAAGCCCTATGATTGCTCATTAGAACCACTCTTAAAAATTTCAAAATATGAT 174
 QY 772 AATAGTTTGAACAAATAACATTTATGCAAGCCTTACAACTATTGTTTGAAGTAGAACAA 831
 DB 173 AACTGTTTAAATAATACAAATGATGCTGCGCACTTATTCTAAGTATTCTAAGTAACTCA 114
 QY 832 GAGATAAGAACTTTCTCGTTTTCAGCTTATTAAATGATAAAAAACACCCCTTTGTTTCTA 888
 DB 113 ATTCTAAGTAATTTGAAAAACATTATCTTCATCTTCAACCTATATGATGTA 57

RESULT 10
 US-09-925-065A-265276
 ; Sequence 265276, Application US/09925065A
 ; Publication No. US20040181048A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single
 ; FILE REFERENCE: 108827.135
 ; CURRENT APPLICATION NUMBER: US/09/925,065A
 ; CURRENT FILING DATE: 2001-08-08

Wed Mar 8 09:11:18 2006

PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 265276
LENGTH: 483
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-597659

Query Match
Best Local Similarity 48.2%; Pred. No. 8.8; DB 6; Length 483;
Matches 109; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 639 AGCAGTCATGAGATGGGAGACCTTCATTCCTCCCAAGCAGAAACGAAATGGAGAGA 698
DB 208 AGAAGCTACTAAGCATATCTATTACACAACTAGAGGAATGAATTAATGGA 267
QY 699 ACAATGAGCCAGAGTTTGAAGAAATAAGATGGTTGATGAAGAGTCGACATAGATT 758
DB 268 ACAAGGAATTTGAACAGGAGACTGAAACAAAGTTGAACAGGAGGAAACAGAAATATT 327
QY 759 GAAAAATACAGAAAATAGTTTGAACAAATAACATTTATGCAAGCCCTTACAACTATTGCT 818
DB 328 GAATAGACAGAGAGCAGTAATGAATTTGAAGCAGTAATTAACAACTACCAAGTCAATA 387
QY 819 TGAAGTAGAACAGAGATAAGAACTTTCCTGTTTCAGCTTATTATA 864
DB 388 AGCCTGAAATGAGAAAGAGGAGCTCTCTTAACATCTATTCTATA 433

RESULT 11
US-09-925-065A-597659
; Sequence 597659, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 597659
; LENGTH: 528
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-597659

Query Match
Best Local Similarity 49.0%; Pred. No. 9.1;
Matches 103; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 36 AACACTGTGTCAAGCTTTCAGGTAGACTGTTTCTTTGGCATGTCCTCGCAACGATTGCA 95

DB 255 ACCACTGAGTCAACCTATATTTCCAAACAAATCTCGAGAAATAGCTCTCGAATACACA 314
QY 96 GACCAAGAACTGGGTGATGCCCATTCCTTGACCCGGCTTGCAGAGACCAAGATCCCTTA 155
DB 315 GACTAAAAAGATGGCGGCTCCCAACCCCAACACCTTCCCTACCCACAGCCCTGTGTC 374
QY 156 AAAGGAAGAGGTAGCACTCTTGCTGTGACATCGAAGCAAGCACTCGTGTGAGAAAGCAG 215
DB 375 AAAATACCCACACACAACTTGAATTTTAAATCTAAGGAAAGAAATCAAGCAGATGAAC 434
QY 216 ATAGTGAGCAGATTCCTGAGAGAGGAATCA 245
DB 435 TGATTGAAGCTTATTTTGTATAGCAATGA 464

RESULT 12
US-09-925-065A-279044/c
; Sequence 279044, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 279044
; LENGTH: 549
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-279044

Query Match
Best Local Similarity 4.3%; Score 38.4; DB 6; Length 549;
Matches 96; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 576 GCCTTAAATGGAATGATTAATACGGTTAGAACTCTGAAACTCTACAGATTCGCTTGG 635
DB 193 GCATTAACTTGGATTATGATAGTGGTTTATCTAAATATCTCCAGTGGTTGTTGA 134
QY 636 AGAAGCAGTCATGAGATGGGAGACCTTCATTCCTCCAAAGCAGAAACGAAATCGAG 695
DB 133 AGAATTAAGTCTATATTTAGAAAAATTTGTAATGAAAAATTAACACTTATTATTTC 74
QY 696 AGAACAATTTGAGCCAGAGTTTGAAGAAATAAGATGGTTGATTGAAGAGTGCACATAG 755
DB 73 AGCAGTATATCTATATTTCTTCCAAAGAAAGAAATCTGAGTGTCTTGAGAGTTGTGCTATTG 14
QY 756 ATTGAAAAATAC 767
DB 13 ACCAGAAATTC 2

RESULT 13
US-09-925-065A-279045/c
; Sequence 279045, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single

;; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
;; FILE REFERENCE: 108827.135
;; CURRENT APPLICATION NUMBER: US/09/925,065A
;; CURRENT FILING DATE: 2001-08-08
;; PRIOR APPLICATION NUMBER: US 60/243,096
;; PRIOR FILING DATE: 2000-10-24
;; PRIOR APPLICATION NUMBER: US 60/252,147
;; PRIOR FILING DATE: 2000-11-20
;; PRIOR APPLICATION NUMBER: US 60/250,092
;; PRIOR FILING DATE: 2000-11-30
;; PRIOR APPLICATION NUMBER: US 60/261,766
;; PRIOR FILING DATE: 2001-01-16
;; PRIOR APPLICATION NUMBER: US 60/289,846
;; PRIOR FILING DATE: 2001-05-09
;; NUMBER OF SEQ ID NOS: 957086
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 279045
;; LENGTH: 549
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; US-09-925-065A-279045

Query Match 4.3%; Score 38.4; DB 6; Length 549;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 96; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
QY 576 GGACTTAATGAATGATAACGGTTAGAACTCTCGAACTCTACAGAGATTGCTTGG 635
DB 193 GGATTAACTTGGATTATGATAGTGGTTTATTATCTTAATTCTCCAGTGGTTGTTGA 134
QY 636 AGAAGCAGTCATGAGAAATGAGAGACCTTCATCCCTCCAAAGCAGAAACGAAATGGAG 695
DB 133 AGATTAAAGTCATATTAGAAAAATTTGTAATGGAATAAATACACTTATTATATTC 74
QY 696 AGAACAATTGAGCAGAGAGTTTGAAGAAATAAGATGTTGATTGAAGAGTGGCAGATAG 755
DB 73 AGGCAGTACTATATTTCTTCCAAAGAGATGTCAGTGTCTTTCAGAGTTGTGTCATTG 14
QY 756 ATTGAAATATAC 767
DB 13 AACCGAATTC 2

RESULT 14
US-09-925-065A-766520
; Sequence 766520, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 766520
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-766520

Query Match 4.3%; Score 38.4; DB 6; Length 623;

Best Local Similarity 53.3%; Pred. No. 12;
Matches 81; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
QY 644 TCATGAGATGGAGACCTTCATTCCCTCCAAAGCAGAAACGAAATCGAGAGACAAT 703
DB 174 TTATGAAATTCBAACCTTTTGTCTGTGAAGACAGCATTTGAGAAACGAAAGCACAAG 233
QY 704 TGAGCCGAGAGATTTGAAGAAATAAGATGTTGATTGAAGAGTCCGACATAGATTGAAAA 763
DB 234 CCAGACACTTGGTTAAAGTATATGTTGATAAAAGATGTATCCAGTATATATAATAA 293
QY 764 ATACAGAAATAGTTTGAACAAATAACATTT 795
DB 294 CTCTTAATCTCAGCAATAAACAACAACACTTT 325

RESULT 15
US-09-925-065A-771317
; Sequence 771317, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 771317
; LENGTH: 631
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-771317

Query Match 4.3%; Score 38.4; DB 6; Length 631;
Best Local Similarity 53.3%; Pred. No. 12;
Matches 81; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
QY 644 TCATGAGATGGAGACCTTCATTCCCTCCAAAGCAGAAACGAAATCGAGAGACAAT 703
DB 182 TTATGAAATTCBAACCTTTTGTCTGTGAAGACAGCATTTGAGAAACGAAAGCACAAG 241
QY 704 TGAGCCGAGAGATTTGAAGAAATAAGATGTTGATTGAAGAGTCCGACATAGATTGAAAA 763
DB 242 CCAGACACTTGGTTAAAGTATATGTTGATAAAAGATGTATCCAGTATATATAATAA 301
QY 764 ATACAGAAATAGTTTGAACAAATAACATTT 795
DB 302 CTCTTAATCTCAGCAATAAACAACAACACTTT 333

Search completed: March 8, 2006, 01:39:33
Job time : 418.426 secs

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Db 61 CGATTTCAGACCAAGAACTGGGTGATGCCCCATTCCTTGACCGGCTTCGCCGAGACGAG 120
Qy 121 AAGTCCCTAAAAGCAAGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTCGTGCA 180
Db 121 AAGTCCCTAAAAGCAAGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTCGTGCA 180
Qy 181 GGAAGCAGATAGTGGAGCAGATTCTGGNAGAGGAAATCAGATGAGGCACTTAAATGACC 240
Db 181 GGAAGCAGATAGTGGAGCAGATTCTGGNAGAGGAAATCAGATGAGGCACTTAAATGACC 240
Qy 241 ATTGCCTCTGTCTGCTTCAAGCTACCTTAAGTACATGATGAGTGTCAAGA 300
Db 241 ATTGCCTCTGTCTGCTTCAAGCTACCTTAAGTACATGATGAGTGTCAAGA 300
Qy 301 GACTGTTTCACTGCTCATGCCCCAAGCAGAAAGTAAAGAGGCTCCCTATGATAGATGAGC 360
Db 301 GACTGTTTCACTGCTCATGCCCCAAGCAGAAAGTAAAGAGGCTCCCTATGATAGATGAGC 360
Qy 361 CAGGCAATCATGGATTAAGAAATCACTAATTAAGCAAACTTTAGTGTGATTTTGAAGG 420
Db 361 CAGGCAATCATGGATTAAGAAATCACTAATTAAGCAAACTTTAGTGTGATTTTGAAGG 420
Qy 421 CTGGAGACAATACTACTTAGAGGCTTTCACCGAAGAGAGGAGCTGCTTGGCGAAAT 480
Db 421 CTGGAGACAATACTACTTAGAGGCTTTCACCGAAGAGAGGAGCTGCTTGGCGAAAT 480
Qy 481 TCACCATTCCTCTCTCCAGGACATATAATGAGGATGTCAAAATGCAATTTGGGTC 540
Db 481 TCACCATTCCTCTCTCCAGGACATATAATGAGGATGTCAAAATGCAATTTGGGTC 540
Qy 541 CTATCGGAGGACTTAAATGGAATGATATACGGTTAGAAATCTCTGAAACTCTACAGAGA 600
Db 541 CTATCGGAGGACTTAAATGGAATGATATACGGTTAGAAATCTCTGAAACTCTACAGAGA 600
Qy 601 TTGCTTGGAGAGCAGTCAATGGAATGGGAGACCTTCAATCCCTCCAAAGCAGAAACGA 660
Db 601 TTGCTTGGAGAGCAGTCAATGGAATGGGAGACCTTCAATCCCTCCAAAGCAGAAACGA 660
Qy 661 AAAATGGAGAGCAAAATGAGCCAGAGTT 690
Db 661 AAAATGGAGAGCAAAATGAGCCAGAGTT 690

RESULT 6
US-10-181-585B-41
; Sequence 41, Application US/10181585B
; Publication No. US20050175985A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System
; APPLICANT: Of Higher Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C3-PUS
; CURRENT APPLICATION NUMBER: US/10/181,585B
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: PCT/US01/05048
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/506,286
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-181-585B-41

Query Match 100.0%; Score 690; DB 9; Length 690;
Best Local Similarity 100.0%; Pred. No. 1.4e-206;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGATTCACACACTGTGTCAAGCTTTCAAGGTAGACTGTGTTCTTTGGCATGTCCGCAAA 60
Db 1 ATGGATTCACACACTGTGTCAAGCTTTCAAGGTAGACTGTGTTCTTTGGCATGTCCGCAAA 60
Qy 61 CGATTTTCAGAGCAAGAACTGGGTGATGCCCAATTCCTTGAACGGCTTCGCCGAGACGAG 120
Db 61 CGATTTTCAGAGCAAGAACTGGGTGATGCCCAATTCCTTGAACGGCTTCGCCGAGACGAG 120
Qy 121 AAGTCCCTAAAAGCAAGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTCGTGCA 180
Db 121 AAGTCCCTAAAAGCAAGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTCGTGCA 180
Qy 181 GGAAGCAGATAGTGGAGCAGATTCTGGNAGAGGAAATCAGATGAGGCACTTAAATGACC 240
Db 181 GGAAGCAGATAGTGGAGCAGATTCTGGNAGAGGAAATCAGATGAGGCACTTAAATGACC 240
Qy 241 ATTGCCTCTGTCTGCTTCAAGCTACCTTAAGTACATGATGAGTGTCAAGA 300
Db 241 ATTGCCTCTGTCTGCTTCAAGCTACCTTAAGTACATGATGAGTGTCAAGA 300
Qy 301 GACTGTTTCACTGCTCATGCCCCAAGCAGAAAGTAAAGAGGCTCCCTATGATAGATGAGC 360
Db 301 GACTGTTTCACTGCTCATGCCCCAAGCAGAAAGTAAAGAGGCTCCCTATGATAGATGAGC 360
Qy 361 CAGGCAATCATGGATTAAGAAATCACTAATTAAGCAAACTTTAGTGTGATTTTGAAGG 420
Db 361 CAGGCAATCATGGATTAAGAAATCACTAATTAAGCAAACTTTAGTGTGATTTTGAAGG 420
Qy 421 CTGGAGACAATACTACTTAGAGGCTTTCACCGAAGAGAGGAGCTGCTTGGCGAAAT 480
Db 421 CTGGAGACAATACTACTTAGAGGCTTTCACCGAAGAGAGGAGCTGCTTGGCGAAAT 480
Qy 481 TCACCATTCCTCTCTCCAGGACATATAATGAGGATGTCAAAATGCAATTTGGGTC 540
Db 481 TCACCATTCCTCTCTCCAGGACATATAATGAGGATGTCAAAATGCAATTTGGGTC 540
Qy 541 CTATCGGAGGACTTAAATGGAATGATATACGGTTAGAAATCTCTGAAACTCTACAGAGA 600
Db 541 CTATCGGAGGACTTAAATGGAATGATATACGGTTAGAAATCTCTGAAACTCTACAGAGA 600
Qy 601 TTGCTTGGAGAGCAGTCAATGGAATGGGAGACCTTCAATCCCTCCAAAGCAGAAACGA 660
Db 601 TTGCTTGGAGAGCAGTCAATGGAATGGGAGACCTTCAATCCCTCCAAAGCAGAAACGA 660
Qy 661 AAAATGGAGAGCAAAATGAGCCAGAGTT 690
Db 661 AAAATGGAGAGCAAAATGAGCCAGAGTT 690

RESULT 7
US-10-065-133A-53
; Sequence 53, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-53

Query Match 100.0%; Score 690; DB 6; Length 888;

Best Local Similarity 100.0%; Pred. No. 1.6e-206;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATTCCAAACACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCGCGCAA 60
DB 25 ATGATTCCAAACACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCGCGCAA 84
QY 61 CGATTTCGAGACCAAGAACTGGGTGATGCCCATCTTCTGACCGGCTTCGCGGAGACCG 120
DB 85 CGATTTCGAGACCAAGAACTGGGTGATGCCCATCTTCTGACCGGCTTCGCGGAGACCG 144
QY 121 AAGTCCCTTAAAGGAAGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTTCGTGCA 180
DB 145 AAGTCCCTTAAAGGAAGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTTCGTGCA 204
QY 181 GGAAGACAGATAGTGGAGCAGATCTCTGGAAGAGGAATCAGATGAGGCACTTAAAGTACC 240
DB 205 GGAAGACAGATAGTGGAGCAGATCTCTGGAAGAGGAATCAGATGAGGCACTTAAAGTACC 264
QY 241 ATTGCTCTGTCTCTGCTTCAAGCTTAACTGACATGACTCTTGTGAGATGTCAGA 300
DB 265 ATTGCTCTGTCTCTGCTTCAAGCTTAACTGACATGACTCTTGTGAGATGTCAGA 324
QY 301 GACTGGTTCATGCTCATGCTGCTTCAAGCAGAAAGTAACTGAGGCTTCCCTATGTAAGAAATGGAC 360
DB 325 GACTGGTTCATGCTCATGCTGCTTCAAGCAGAAAGTAACTGAGGCTTCCCTATGTAAGAAATGGAC 384
QY 361 CAGGCAATCATGATAGAAACATCATCTTAAAGCAAACTTTAGTGTGATTTTTCGAAAGG 420
DB 385 CAGGCAATCATGATAGAAACATCATCTTAAAGCAAACTTTAGTGTGATTTTTCGAAAGG 444
QY 421 CTGGAGACATTAATCTTCTGAGGCTTCAAGCAAGAGGAGGAGTCTGTTGGCGAAAT 480
DB 445 CTGGAGACATTAATCTTCTGAGGCTTCAAGCAAGAGGAGGAGTCTGTTGGCGAAAT 504
QY 481 TCACCATTTGCTTCTCTTCAGGACATATCTGAGGATGTCAGAAATGCAATTTGGGGTC 540
DB 505 TCACCATTTGCTTCTCTTCAGGACATATCTGAGGATGTCAGAAATGCAATTTGGGGTC 564
QY 541 CTCATCGGAGACTTAAATGGAATGATTAATGAGTCTCTGAACTCTACAGAGA 600
DB 565 CTCATCGGAGACTTAAATGGAATGATTAATGAGTCTCTGAACTCTACAGAGA 624
QY 601 TTCGCTTGGAGAGCAGTCTATGAGATGGAGACCTTCAATCCCTCCAAAGCAGAAACGA 660
DB 625 TTCGCTTGGAGAGCAGTCTATGAGATGGAGACCTTCAATCCCTCCAAAGCAGAAACGA 684
QY 661 AAAATGGAGAGACAAATTTGAGCCAGAGTT 690
DB 685 AAAATGGAGAGACAAATTTGAGCCAGAGTT 714

RESULT 8
US-10-065-133A-57
; Sequence 57, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 57
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8

FEATURE:
; NAME/KEY: CDS
; LOCATION: (27)...(716)
; OTHER INFORMATION:
US-10-065-133A-57

Query Match 100.0%; Score 690; DB 6; Length 888;
Best Local Similarity 100.0%; Pred. No. 1.6e-206;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATTTCACCACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCGCGCAA 60
DB 27 ATGATTTCACCACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCGCGCAA 86
QY 61 CGATTTCGAGACCAAGAACTGGGTGATGCCCATCTTCTGACCGGCTTCGCGGAGACCG 120
DB 87 CGATTTCGAGACCAAGAACTGGGTGATGCCCATCTTCTGACCGGCTTCGCGGAGACCG 146
QY 121 AAGTCCCTTAAAGGAAGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTTCGTGCA 180
DB 147 AAGTCCCTTAAAGGAAGAGGTAGCACTCTTGGTCTGGACATCGAAACAGCCACTTCGTGCA 206
QY 181 GGAAGACAGATAGTGGAGCAGATCTTGGAAAGAGGAATCAGATGAGGCACTTAAAGTACC 240
DB 207 GGAAGACAGATAGTGGAGCAGATCTTGGAAAGAGGAATCAGATGAGGCACTTAAAGTACC 266
QY 241 ATTGCTCTGTCTCTGCTTCAAGCTTAACTGACATGACTCTTGTGAGATGTCAGA 300
DB 267 ATTGCTCTGTCTCTGCTTCAAGCTTAACTGACATGACTCTTGTGAGATGTCAGA 326
QY 301 GACTGGTTCATGCTCATGCTGCTTCAAGCAGAAAGTAACTGAGGCTTCCCTATGTAAGAAATGGAC 360
DB 327 GACTGGTTCATGCTCATGCTGCTTCAAGCAGAAAGTAACTGAGGCTTCCCTATGTAAGAAATGGAC 386
QY 361 CAGGCAATCATGATAGAAACATCATCTTAAAGCAAACTTTAGTGTGATTTTTCGAAAGG 420
DB 387 CAGGCAATCATGATAGAAACATCATCTTAAAGCAAACTTTAGTGTGATTTTTCGAAAGG 446
QY 421 CTGGAGACATTAATCTTCTGAGGCTTCAAGCAAGAGGAGGAGTCTGTTGGCGAAAT 480
DB 447 CTGGAGACATTAATCTTCTGAGGCTTCAAGCAAGAGGAGGAGTCTGTTGGCGAAAT 506
QY 481 TCACCATTTGCTTCTCTTCAGGACATATCTGAGGATGTCAGAAATGCAATTTGGGGTC 540
DB 507 TCACCATTTGCTTCTCTTCAGGACATATCTGAGGATGTCAGAAATGCAATTTGGGGTC 566
QY 541 CTCATCGGAGACTTAAATGGAATGATTAATGAGTCTCTGAACTCTACAGAGA 600
DB 567 CTCATCGGAGACTTAAATGGAATGATTAATGAGTCTCTGAACTCTACAGAGA 626
QY 601 TTCGCTTGGAGAGCAGTCTATGAGATGGAGACCTTCAATCCCTCCAAAGCAGAAACGA 660
DB 627 TTCGCTTGGAGAGCAGTCTATGAGATGGAGACCTTCAATCCCTCCAAAGCAGAAACGA 686
QY 661 AAAATGGAGAGACAAATTTGAGCCAGAGTT 690
DB 687 AAAATGGAGAGACAAATTTGAGCCAGAGTT 716

RESULT 9
US-10-734-373-53
; Sequence 53, Application US/10734373
; Publication No. US20040137015A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/734,373
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921

;; PRIOR FILING DATE: 1998-08-13
;; NUMBER OF SEQ ID NOS: 108
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 53
;; LENGTH: 888
;; TYPE: DNA
;; ORGANISM: Equine influenza virus H3N8
US-10-734-373-59

Query Match 100.0%; Score 690; DB 7; Length 888;
Best Local Similarity 100.0%; Pred. No. 1.6e-206; Indels 0; Gaps 0;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGATTCACACATGCTCAAGCTTTCAGGTAGACTGTTTCTTGGCATGTCCGCAA 60
DB 25 ATGGATTCACACATGCTCAAGCTTTCAGGTAGACTGTTTCTTGGCATGTCCGCAA 84
QY 61 CGATTTGCGAGCAAGAACTGGGTGATGCCATTCCTTGCAGCGGTTCCGCGAGCAG 120
DB 85 CGATTTGCGAGCAAGAACTGGGTGATGCCATTCCTTGCAGCGGTTCCGCGAGCAG 144
QY 121 AAGTCCCTAAAAGGAGAGGTAGCACTCTTGGTCTGAGCATCGAAACAGCCACTCGTGCA 180
DB 145 AAGTCCCTAAAAGGAGAGGTAGCACTCTTGGTCTGAGCATCGAAACAGCCACTCGTGCA 204
QY 181 GGAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGCACTTAAATGACC 240
DB 205 GGAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGCACTTAAATGACC 264
QY 241 ATTGCTCTGTTCTTCTGCTTACGCTACTTAACCTGACATGACTCTTGTGAGATGTCAGA 300
DB 265 ATTGCTCTGTTCTTCTGCTTACGCTACTTAACCTGACATGACTCTTGTGAGATGTCAGA 324
QY 301 GACTGGTTCATGCTCATGCCCAGCAAGAAAGTAAACAGGCTCCCTATGTATATAAGAAAGG 360
DB 325 GACTGGTTCATGCTCATGCCCAGCAAGAAAGTAAACAGGCTCCCTATGTATATAAGAAAGG 384
QY 361 CAGCAATCATGTAAGAAACATCATACTTAAAGCAAACTTTAGTGTGATTTTCAAAGG 420
DB 385 CAGCAATCATGTAAGAAACATCATACTTAAAGCAAACTTTAGTGTGATTTTCAAAGG 444
QY 421 CTGGAGACACTAATACTACTTAGAGCCTTCAACGAAGAGGAGCAGTCGTTGGCAAAAT 480
DB 445 CTGGAGACACTAATACTACTTAGAGCCTTCAACGAAGAGGAGCAGTCGTTGGCAAAAT 504
QY 481 TCACCATTCCTTCTTCCAGGACATCTAATGAGGATGTCAAAAATGCAATTTGGGGTC 540
DB 505 TCACCATTCCTTCTTCCAGGACATCTAATGAGGATGTCAAAAATGCAATTTGGGGTC 564
QY 541 CTGATCGGAGCACTTAATGGAATGATATACGGTTAGAACTCTGAACTCTACAGAGA 600
DB 565 CTGATCGGAGCACTTAATGGAATGATATACGGTTAGAACTCTGAACTCTACAGAGA 624
QY 601 TTCCCTTGGAGAGCAGTCATGAGAAATGGAGACCTTCAATTCCTCCCAAGCAGAAACGA 660
DB 625 TTCCCTTGGAGAGCAGTCATGAGAAATGGAGACCTTCAATTCCTCCCAAGCAGAAACGA 684
QY 661 AAATGGAGAGCAATTTGAGCCAGAAAGTT 690
DB 685 AAATGGAGAGCAATTTGAGCCAGAAAGTT 714

RESULT 10
US-10-734-373-57
; Sequence 57, Application US/10734373
; Publication No. US20040137015A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/734,373
; CURRENT FILING DATE: 2003-12-12

;; PRIOR APPLICATION NUMBER: PCT/US99/18583
;; PRIOR FILING DATE: 1999-08-12
;; PRIOR APPLICATION NUMBER: 09/133,921
;; PRIOR FILING DATE: 1998-08-13
;; NUMBER OF SEQ ID NOS: 108
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 57
;; LENGTH: 888
;; TYPE: DNA
;; ORGANISM: Equine influenza virus H3N8
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (27)..(716)
;; OTHER INFORMATION:
US-10-734-373-57

Query Match 100.0%; Score 690; DB 7; Length 888;
Best Local Similarity 100.0%; Pred. No. 1.6e-206; Indels 0; Gaps 0;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGATTCACACATGCTCAAGCTTTCAGGTAGACTGTTTCTTGGCATGTCCGCAA 60
DB 27 ATGGATTCACACATGCTCAAGCTTTCAGGTAGACTGTTTCTTGGCATGTCCGCAA 86
QY 61 CGATTTGCGAGCAAGAACTGGGTGATGCCATTCCTTGCAGCGGTTCCGCGAGCAG 120
DB 87 CGATTTGCGAGCAAGAACTGGGTGATGCCATTCCTTGCAGCGGTTCCGCGAGCAG 146
QY 121 AAGTCCCTAAAAGGAGAGGTAGCACTCTTGGTCTGAGCATCGAAACAGCCACTCGTGCA 180
DB 147 AAGTCCCTAAAAGGAGAGGTAGCACTCTTGGTCTGAGCATCGAAACAGCCACTCGTGCA 206
QY 181 GGAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGCACTTAAATGACC 240
DB 207 GGAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGCACTTAAATGACC 266
QY 241 ATTGCTCTGTTCTTCTGCTTACGCTACTTAACTGACATGACTCTTGTGAGATGTCAGA 300
DB 267 ATTGCTCTGTTCTTCTGCTTACGCTACTTAACTGACATGACTCTTGTGAGATGTCAGA 326
QY 301 GACTGGTTCATGCTCATGCCCAGCAAGAAAGTAAACAGGCTCCCTATGTATATAAGAAAGG 360
DB 327 GACTGGTTCATGCTCATGCCCAGCAAGAAAGTAAACAGGCTCCCTATGTATATAAGAAAGG 386
QY 361 CAGGCAATCATGTAAGAAACATCATACTTAAAGCAAACTTTAGTGTGATTTTCAAAGG 420
DB 387 CAGGCAATCATGTAAGAAACATCATACTTAAAGCAAACTTTAGTGTGATTTTCAAAGG 446
QY 421 CTGGAGACACTAATACTACTTAGAGCCTTCAACGAAGAGGAGCAGTCGTTGGCAAAAT 480
DB 447 CTGGAGACACTAATACTACTTAGAGCCTTCAACGAAGAGGAGCAGTCGTTGGCAAAAT 506
QY 481 TCACCATTCCTTCTTCCAGGACATCTAATGAGGATGTCAAAAATGCAATTTGGGGTC 540
DB 507 TCACCATTCCTTCTTCCAGGACATCTAATGAGGATGTCAAAAATGCAATTTGGGGTC 566
QY 541 CTGATCGGAGCACTTAATGGAATGATATACGGTTAGAACTCTGAACTCTACAGAGA 600
DB 567 CTGATCGGAGCACTTAATGGAATGATATACGGTTAGAACTCTGAACTCTACAGAGA 626
QY 601 TTCCCTTGGAGAGCAGTCATGAGAAATGGAGACCTTCAATTCCTCCCAAGCAGAAACGA 660
DB 627 TTCCCTTGGAGAGCAGTCATGAGAAATGGAGACCTTCAATTCCTCCCAAGCAGAAACGA 686
QY 661 AAATGGAGAGCAATTTGAGCCAGAAAGTT 690
DB 687 AAATGGAGAGCAATTTGAGCCAGAAAGTT 716

RESULT 11
US-10-181-585B-35
; Sequence 35, Application US/10181585B
; Publication No. US20050175965A1


```

; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System
; APPLICANT: of Higher Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C3-PUS
; CURRENT APPLICATION NUMBER: US/10/181.585B
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: PCT/US01/05048
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/506,286
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-181-585B-35

Query Match      100.0%; Score 690; DB 9; Length 888;
Best Local Similarity 100.0%; Pred. No. 1.6e-206;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ATGGATTCCAACTGTGTCAAGCTTTCAGGTAGACTGTTTCTTTGGCATGTCCGCAA 60
Db      25  ATGGATTCCAACTGTGTCAAGCTTTCAGGTAGACTGTTTCTTTGGCATGTCCGCAA 84

Qy      61  CGATTTCGAGACCAAGACTGGGTGATGCCCCATTCCTTGACCGGCTTCGCCGAGACCA 120
Db      85  CGATTTCGAGACCAAGACTGGGTGATGCCCCATTCCTTGACCGGCTTCGCCGAGACCA 144

Qy      121  AAGTCCCTTAAAGGAAGAGGTAGACTCTTGGTCTGACATCGAAACAGGCACTCGTGCA 180
Db      145  AAGTCCCTTAAAGGAAGAGGTAGACTCTTGGTCTGACATCGAAACAGGCACTCGTGCA 204

Qy      181  GGAAGCAGATAGTGGAGCAGATCTCGGAGAGGATTCAGATGAGGCACTTAAATGACC 240
Db      205  GGAAGCAGATAGTGGAGCAGATCTCGGAGAGGATTCAGATGAGGCACTTAAATGACC 264

Qy      241  ATTGCTCTGTTCTGCTTCAAGCTTCACTTAACTGACATGACCTCTTGTAGATGATGCA 300
Db      265  ATTGCTCTGTTCTGCTTCAAGCTTCACTTAACTGACATGACCTCTTGTAGATGATGCA 324

Qy      301  GACTGGTTCATGCTGATGCCGAGCAGAAAGTAAACAGCACTTGTAGTGTGATTTGAAAG 360
Db      325  GACTGGTTCATGCTGATGCCGAGCAGAAAGTAAACAGCACTTGTAGTGTGATTTGAAAG 384

Qy      361  CAGGCAATCATGGATTAAGAAATCATCTTAAAGCAAACTTTAGTGTGATTTGAAAGG 420
Db      385  CAGGCAATCATGGATTAAGAAATCATCTTAAAGCAAACTTTAGTGTGATTTGAAAGG 444

Qy      421  CTGGAGACATTAATCTTCTAGAGCTTCAACGAGAGGAGGAGTGTGGGCAAAAT 480
Db      445  CTGGAGACATTAATCTTCTAGAGCTTCAACGAGAGGAGGAGTGTGGGCAAAAT 504

Qy      481  TCACCATTTGCTTCTCTTCCAGGACATCTAATGAGGATGTCAAAATGCAATTTGGGGTC 540
Db      505  TCACCATTTGCTTCTCTTCCAGGACATCTAATGAGGATGTCAAAATGCAATTTGGGGTC 564

Qy      541  CTCTCGGAGACTTAAATGGAATGATAATACGGTTAGAACTCTTGAATCTTACAGAGA 600
Db      565  CTCTCGGAGACTTAAATGGAATGATAATACGGTTAGAACTCTTGAATCTTACAGAGA 624

Qy      601  TTCCGCTTGGAGAGCAGTCTAGAAATGGGAGACCTTCACTCCCTCCAAAGCAGAAAC 660
Db      625  TTCCGCTTGGAGAGCAGTCTAGAAATGGGAGACCTTCACTCCCTCCAAAGCAGAAAC 684

Qy      661  AATATGGAGAGCAATTTGAGCCAGAGTT 690
Db      685  AATATGGAGAGCAATTTGAGCCAGAGTT 714
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RESULT 12
US-10-181-585B-39
; Sequence 39, Application US/10181585B
; Publication No. US20050175985A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System
; APPLICANT: of Higher Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C3-PUS
; CURRENT APPLICATION NUMBER: US/10/181.585B
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: PCT/US01/05048
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/506,286
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27)..(716)
US-10-181-585B-39
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Query Match      100.0%; Score 690; DB 9; Length 888;
Best Local Similarity 100.0%; Pred. No. 1.6e-206;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ATGGATTCCAACTGTGTCAAGCTTTCAGGTAGACTGTTTCTTTGGCATGTCCGCAA 60
Db      27  ATGGATTCCAACTGTGTCAAGCTTTCAGGTAGACTGTTTCTTTGGCATGTCCGCAA 86

Qy      61  CGATTTCGAGACCAAGACTGGGTGATGCCCCATTCCTTGACCGGCTTCGCCGAGACCA 120
Db      87  CGATTTCGAGACCAAGACTGGGTGATGCCCCATTCCTTGACCGGCTTCGCCGAGACCA 146

Qy      121  AAGTCCCTTAAAGGAAGAGGTAGACTCTTGGTCTGACATCGAAACAGGCACTCGTGCA 180
Db      147  AAGTCCCTTAAAGGAAGAGGTAGACTCTTGGTCTGACATCGAAACAGGCACTCGTGCA 206

Qy      181  GGAAGCAGATAGTGGAGCAGATCTCGGAGAGGATTCAGATGAGGCACTTAAATGACC 240
Db      207  GGAAGCAGATAGTGGAGCAGATCTCGGAGAGGATTCAGATGAGGCACTTAAATGACC 266

Qy      241  ATTGCTCTGTTCTGCTTCAAGCTTCACTTAACTGACATGACCTCTTGTAGATGATGCA 300
Db      267  ATTGCTCTGTTCTGCTTCAAGCTTCACTTAACTGACATGACCTCTTGTAGATGATGCA 326

Qy      301  GACTGGTTCATGCTGATGCCGAGCAGAAAGTAAACAGCACTTGTAGTGTGATTTGAAAG 360
Db      327  GACTGGTTCATGCTGATGCCGAGCAGAAAGTAAACAGCACTTGTAGTGTGATTTGAAAG 386

Qy      361  CAGGCAATCATGGATTAAGAAATCATCTTAAAGCAAACTTTAGTGTGATTTGCAAAAG 420
Db      387  CAGGCAATCATGGATTAAGAAATCATCTTAAAGCAAACTTTAGTGTGATTTGCAAAAG 446

Qy      421  CTGGAGACATTAATCTTCTAGAGCTTCAACGAGAGGAGGAGTGTGGGCAAAAT 480
Db      447  CTGGAGACATTAATCTTCTAGAGCTTCAACGAGAGGAGGAGTGTGGGCAAAAT 506

Qy      481  TCACCATTTGCTTCTCTTCCAGGACATCTAATGAGGATGTCAAAATGCAATTTGGGGTC 540
Db      507  TCACCATTTGCTTCTCTTCCAGGACATCTAATGAGGATGTCAAAATGCAATTTGGGGTC 566

Qy      541  CTCTCGGAGACTTAAATGGAATGATAATACGGTTAGAACTCTTGAATCTTACAGAGA 600
Db      567  CTCTCGGAGACTTAAATGGAATGATAATACGGTTAGAACTCTTGAATCTTACAGAGA 626
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QY 601 TTGCTTGGAGAGCAGTCATGAGATGGAGAGCCTTCAATCCCTCCAAAGCAGAAACGA 660
Db 627 TTGCTTGGAGAGCAGTCATGAGATGGAGAGCCTTCAATCCCTCCAAAGCAGAAACGA 686
QY 661 AAAAAATGGAGAGCAAAATTTGAGCCAGAGATT 690
Db 687 AAAAAATGGAGAGCAAAATTTGAGCCAGAGATT 716
RESULT 13
US-10-065-133A-50
; Sequence 50, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 50
; LENGTH: 891
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27)..(716)
; OTHER INFORMATION:
US-10-065-133A-50
Query Match 100.0%; Score 690; DB 6; Length 891;
Best Local Similarity 100.0%; Pred. No. 1.6e-206;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGATTCCAAACACTGTGTCAAGCTTTTCAGGTAGACTGTCTTTTGGCATGTCGCGAAA 60
Db 27 ATGGATTCCAAACACTGTGTCAAGCTTTTCAGGTAGACTGTCTTTTGGCATGTCGCGAAA 86
QY 61 CGATTTGCAGACCAAGAACTGGGTGATGCCCATTCCTTTGACCGGCTTCGCCGAGACCAG 120
Db 87 CGATTTGCAGACCAAGAACTGGGTGATGCCCATTCCTTTGACCGGCTTCGCCGAGACCAG 146
QY 121 AAGTCCCTTAAAGGAGAGTAGCACTCTTTGGTCTGGACATCGAAACAGCCACTCGTGCA 180
Db 147 AAGTCCCTTAAAGGAGAGTAGCACTCTTTGGTCTGGACATCGAAACAGCCACTCGTGCA 206
QY 181 GGAAGCAGATAGTGGAGCAGATTCGAGAGGATCAGATGAGGCATTTAAATGACC 240
Db 207 GGAAGCAGATAGTGGAGCAGATTCGAGAGGATCAGATGAGGCATTTAAATGACC 266
QY 241 ATTGCTCTGCTTCCGCTTCAAGCTTAAAGCAAACTTTAGTGTGATTTTCGAAGG 300
Db 267 ATTGCTCTGCTTCCGCTTCAAGCTTAAAGCAAACTTTAGTGTGATTTTCGAAGG 326
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RESULT 14
US-10-734-373-50
; Sequence 50, Application US/10734373
; Publication No. US20040137015A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/734,373
; PRIOR FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 50
; LENGTH: 891
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27)..(716)
; OTHER INFORMATION:
US-10-734-373-50
Query Match 100.0%; Score 690; DB 7; Length 891;
Best Local Similarity 100.0%; Pred. No. 1.6e-206;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 87 CGATTTGCAGACCAAGAACTGGGTGATGCCCATTCCTTTGACCGGCTTCGCCGAGACCAG 146
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Db 567 CTCATCGGAGACTTAAATGGAATGATAATACGGTTAGAACTCTGAAACTCTACAGAGA 626
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Db 687 AAAATGGAGAGCAATTCAGCCAGAGTT 716

RESULT 15

US-10-181-585B-32
; Sequence 32, Application US/10181585B
; Publication No. US20050175985A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System
; APPLICANT: of Higher Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C3-PUS
; CURRENT APPLICATION NUMBER: US/10/181.585B
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: PCT/US01/05048
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/506,286
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 891
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27)..(716)
US-10-181-585B-32

Query Match 100.0%; Score 690; DB 9; Length 891;
Best Local Similarity 100.0%; Pred. No. 1.6e-206;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 121 AAGTCCCTAAAGGAAGAGGTAGCACTCTTGGTCTGGACATCGAAAGAGCCACTCTGTGCA 180
Db 147 AAGTCCCTAAAGGAAGAGGTAGCACTCTTGGTCTGGACATCGAAAGAGCCACTCTGTGCA 206
Qy 181 GGAAGCAGATAGTGGAGCAGATTCGAGAGGAAATCAGATGAGGCACTTAAATGACC 240
Db 207 GGAAGCAGATAGTGGAGCAGATTCGAGAGGAAATCAGATGAGGCACTTAAATGACC 266
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Db 267 ATTGCTCTGCTTCCGCTTCACGTACTTAACTGACATGACTCTTGTGATGATGTCAAGA 326
Qy 301 GACTGCTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTTATGTATAGAATGGAC 360
Db 327 GACTGCTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTTATGTATAGAATGGAC 386
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Db 567 CTCATCGGAGACTTAAATGGAATGATAATACGGTTAGAACTCTGAAACTCTACAGAGA 626
Qy 601 TTCGCTTGGAGAGCAGTCATGGAATGGGAGACCTTCATCCCTCCAAAGCAGAAACGA 660
Db 627 TTCGCTTGGAGAGCAGTCATGGAATGGGAGACCTTCATCCCTCCAAAGCAGAAACGA 686
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Db 687 AAAATGGAGAGCAATTCAGCCAGAGTT 716

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Perfect score: 690
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Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888760828 residues

Total number of hits satisfying chosen parameters: 2606114

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	690	100.0	690	3	US-09-506-286B-59
3	690	100.0	690	3	US-10-065-133A-52
4	690	100.0	690	3	US-10-065-133A-59
5	690	100.0	888	3	US-09-506-286B-53
6	690	100.0	888	3	US-09-506-286B-57
7	690	100.0	888	3	US-10-065-133A-53
8	690	100.0	888	3	US-10-065-133A-57
9	690	100.0	891	3	US-09-506-286B-50
10	690	100.0	891	3	US-10-065-133A-50
11	532.4	77.2	906	3	US-10-204-664A-6
12	291.4	42.2	293	3	US-09-506-286B-56
13	291.4	42.2	293	3	US-10-065-133A-56
14	291.4	42.2	468	3	US-09-506-286B-54
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17	212.8	30.8	918	6	PCT-US94-01149-58
18	212	30.7	453	2	US-08-388-267C-3
19	212	30.7	453	3	US-09-277-720-3
20	212	30.7	690	6	PCT-US94-01149-11
21	212	30.7	690	6	PCT-US94-01149-71
22	212	30.7	924	6	PCT-US94-01149-15
23	211.6	30.7	681	6	PCT-US94-01149-25
24	211.6	30.7	717	6	PCT-US94-01149-23

25	211.6	30.7	729	6	PCT-US94-01149-17	Sequence 17, Appl
26	211.6	30.7	912	6	PCT-US94-01149-31	Sequence 31, Appl
27	210.4	30.5	1014	3	US-08-441-857-7	Sequence 7, Appl
28	210.4	30.5	1014	3	US-08-193-159-7	Sequence 7, Appl
29	210.4	30.5	1014	3	US-09-283-646C-7	Sequence 7, Appl
30	210.4	30.5	1017	2	US-08-441-857-9	Sequence 9, Appl
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36	210.4	30.5	1020	2	US-08-441-857-5	Sequence 5, Appl
37	210.4	30.5	1020	3	US-08-193-159-5	Sequence 5, Appl
38	210.4	30.5	1020	3	US-09-283-646C-5	Sequence 5, Appl
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40	208.8	30.3	7616	6	PCT-US94-01149-54	Sequence 54, Appl
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42	112	16.2	830	6	PCT-US94-01149-21	Sequence 21, Appl
43	112	16.2	810	2	PCT-US94-01149-19	Sequence 19, Appl
44	39.4	5.7	7218	2	US-08-232-463-14	Sequence 14, Appl
45	39.2	5.7	601	3	US-09-949-016-152799	Sequence 152799,

ALIGNMENTS

RESULT 1
US-09-506-286B-52
; Sequence 52, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; CURRENT FILING DATE: 2000-02-16
; PRIOR FILING DATE: 1998-08-13
; PRIOR FILING DATE: 1999-08-12
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-09-506-286B-52

Query Match	100.0%	Score 690;	DB 3;	Length 690;
Best Local Similarity	100.0%	Pred. No. 1.6e-212;	Mismatches 0;	Indels 0;
Matches 690;	Conservative 0;			
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QY	241	ATTGCTCTGTTCTCTGCTTCAGCTACTTAACTGACATGACTCTTTCAGATGTCAGAGA	300	
DB	241	ATTGCTCTGTTCTCTGCTTCAGCTACTTAACTGACATGACTCTTTCAGATGTCAGAGA	300	

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DB 301 GACTGGTTCATGCTCATGCCCAAGCAGAAAGTAACAGGCTCCCTATGTATAGAATGGAC 360
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RESULT 2
US-09-506-286B-59
; Sequence 59, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; CURRENT FILING DATE: 2000-02-16
; PRIOR FILING DATE: 09/133,921
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1998-08-13
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-09-506-286B-59
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Query Match 100.0%; Score 690; DB 3; Length 690;
Best Local Similarity 100.0%; Pred. No. 1.6e-212; Indels 0; Gaps 0;
Matches 690; Conservative 0; Mismatches 0;

QY 1 ATGATTCACACATGTGTCAAGCTTTCAGGTAGACTGTCTTTCTTTGGCATGTCCGAAA 60
DB 1 ATGATTCACACATGTGTCAAGCTTTCAGGTAGACTGTCTTTCTTTGGCATGTCCGAAA 60
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DB 61 CGAATTCAGACCAAGAACTGGGTGATGCCCAATTCCTTGACCGGCTTCCCGAGACGAG 120
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DB 121 AAGTCCCTAAAAGGAGAGGTAGCACTCTTGGTCTTGGACATCGAAGAACGCCCACTCGTGCA 180
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DB 181 GGAAGCAGATAGTGAGCAGATTCTTGGAGAGGAAATCAGATGAGGCACTTAAATATGACC 240
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QY 301 GACTGGTTCATGCTCATGCCCAAGCAGAAAGTAACAGGCTCCCTATGTATAGAATGGAC 360
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RESULT 3
US-10-065-133A-52
; Sequence 52, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR FILING DATE: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-52
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Query Match 100.0%; Score 690; DB 3; Length 690;
Best Local Similarity 100.0%; Pred. No. 1.6e-212; Indels 0; Gaps 0;
Matches 690; Conservative 0; Mismatches 0;

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DB 1 ATGGAATTCACACATGTGTCAAGCTTTCAGGTAGACTGTCTTTCTTTGGCATGTCCGAAA 60
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us-10-734-373-59.rni

Wed Mar 8 09:11:20 2006

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625	DB	TTCCGCTTTGGGAGAGCAGTCAATGAGAAATGGGAGACCTTCAATTCCTCCAAAGCAAAACGA	684
661	QY	AAAAATGGAGAGAACAAATTGAGCCAGAAATT	690
685	DB	AAAAATGGAGAGAACAAATTGAGCCAGAAATT	714

RESULT 6

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US-09-506-286B-57
; Sequence 57, Application US/09506286B
; Patent No. 6492414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia S.
; APPLICANT: Townner, Julius S.
; APPLICANT: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; CURRENT FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 57
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27) .. (716)
US-09-506-286B-57

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Matches	690;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
1 Qy	ATGGATTCACACATCTGTCTCAAGCTTTTCAGTAGACTGTTTCTTTGGCATCTCCGCAAA	60							
27 Db	ATGGATTCACACACTGTGTCAAGCTTTCAGTAGACTGTTTCTTTGGCATCTCCGCAAA	86							
61 Qy	CGATTTGCAGACCAAGAACTGGGTGATGCCGATCTCTTGACCGGCTTCGCCGAGACCAAG	120							
87 Db	CGATTTGCAGACCAAGAACTGGGTGATGCCGATCTCTTGACCGGCTTCGCCGAGACCAAG	146							
121 Qy	AAGTCCCTTAAAGGAAGAGGTAGACACTCTTGGTCTGGCACTGCAAAACAGCCACTCGTGCA	180							
147 Db	AAGTCCCTTAAAGGAAGAGGTAGACACTCTTGGTCTGGCACTGCAAAACAGCCACTCGTGCA	206							
181 Qy	GGAAAGCAGATAGTGGAGCAGATCTCTGGAGAGGAATCAGATGAGGCATCTTAAATGACC	240							
207 Db	GGAAAGCAGATAGTGGAGCAGATCTCTGGAGAGGAATCAGATGAGGCATCTTAAATGACC	266							
241 Qy	ATTGCCCTCTGTCTCTGCTTCAACGCTACTTAATCTGACATGCACTCTGTATGAGATGTCAMGA	300							
267 Db	ATTGCCCTCTGTCTCTGCTTCAACGCTACTTAATCTGACATGCACTCTGTATGAGATGTCAMGA	326							
301 Qy	GACTGGGTTCATGCTCATCGCCCAAGCAGAAAGTAACAGGCTCCCTATGTAAGAAGTGCAC	360							
327 Db	GACTGGGTTCATGCTCATCGCCCAAGCAGAAAGTAACAGGCTCCCTATGTAAGAAGTGCAC	386							
361 Qy	CAGGCAATCATCGATAAGAACATCATPACTTAAGAGAACTTTAGTGTGATCTTTGCAAGG	420							
387 Db	CAGGCAATCATCGATAAGAACATCATPACTTAAGAGAACTTTAGTGTGATCTTTGCAAGG	446							
421 Qy	CTGGAGACACTAATACTACTTTAGAGCCTTTCACGAGAGAGAGCAAGTCTGTTGGCGAATT	480							
447 Db	CTGGAGACACTAATACTACTTTAGAGCCTTTCACGAGAGAGAGCAAGTCTGTTGGCGAATT	506							
481 Qy	TCAACATTCGCTTCTCTTCCAGGACATACATAAGAGATGTCAAAAATGCAATGGGGTTC	540							
507 Db	TCAACATTCGCTTCTCTTCCAGGACATACATAAGAGATGTCAAAAATGCAATGGGGTTC	566							
541 Qy	CTCATCGGAGGACTTAAATGGAATGATAATACGGTTAGAACTCTGAAACTCTTACAGAGA	600							
567 Db	CTCATCGGAGGACTTAAATGGAATGATAATACGGTTAGAACTCTGAAACTCTTACAGAGA	626							
601 Qy	TTTCGCTTGGAGAGCAGTTCATGAGAAATGGGAGACTTCAATTCCTCCAAAGCAGAAACGA	660							
627 Db	TTTCGCTTGGAGAGCAGTTCATGAGAAATGGGAGACTTCAATTCCTCCAAAGCAGAAACGA	686							
661 Qy	AAAAATGGAGAGAAACAATTGAGCCAGAGTTT	690							
687 Db	AAAAATGGAGAGAAACAATTGAGCCAGAGTTT	716							

RESULT, T 7

US-10-065-133A-53
 / Sequence 53, Application US/10065133A
 / Patent No. 6685946
 / GENERAL INFORMATION:
 / APPLICANT: Dowling, Patricia W.
 / APPLICANT: Youngner, Julius S.
 / TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
 / FILE REFERENCE: EQ-1-C2-1
 / CURRENT APPLICATION NUMBER: US/10/065,133A
 / CURRENT FILING DATE: 2002-12-10
 / PRIOR APPLICATION NUMBER: PCT/US99/18593
 / PRIOR FILING DATE: 1999-08-12
 / PRIOR APPLICATION NUMBER: 09/133,921
 / PRIOR FILING DATE: 1998-08-13
 / NUMBER OF SEQ ID NOS: 108
 / SOFTWARE: atencin version 3.1
 / SEQ ID NO 53
 / LENGTH: 888
 / TYPE: DNA
 / ORGANISM: Equine influenza virus H3N8
 US-10-065-133A-53

; PRIOR APPLICATION NUMBER: 09/133,921
 ; PRIOR FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: PCT/US99/18583
 ; PRIOR FILING DATE: 1999-08-12
 ; NUMBER OF SEQ ID NOS: 108
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 50
 ; LENGTH: 891
 ; TYPE: DNA
 ; ORGANISM: Equine influenza virus H3N8
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (27)..(716)
 ; US-09-506-286B-50

Query Match 100.0%; Score 690; DB 3; Length 891;
 Best Local Similarity 100.0%; Pred. No. 1.9e-212; Indels 0; Gaps 0;
 Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGGATTCCAACTGTGTCAAGCTTTCAGGTAGACTGTTTCTTTGGCATGTCCGCAAA	60
DB	27	ATGGATTCCAACTGTGTCAAGCTTTCAGGTAGACTGTTTCTTTGGCATGTCCGCAAA	86
QY	61	CGATTTCGACGACCAAGAACTGGGTGATGCCCATTCCTTGACCGGCTTCGCCGAGACG	120
DB	87	CGATTTCGACGACCAAGAACTGGGTGATGCCCATTCCTTGACCGGCTTCGCCGAGACG	146
QY	121	AAGTCCCTTAAAGAGAGAGTGTGATGCTTGGTCTGGACATCGAACAAGCCACTCGTGCA	180
DB	147	AAGTCCCTTAAAGAGAGAGTGTGATGCTTGGTCTGGACATCGAACAAGCCACTCGTGCA	206
QY	181	GGAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGGCACCTTAAATGACC	240
DB	207	GGAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGGCACCTTAAATGACC	266
QY	241	ATTGCTCTGTTCTCTGCTTACGCTACTTAACTGACATGATCTTTGATGAGATGTCAAGA	300
DB	267	ATTGCTCTGTTCTCTGCTTACGCTACTTAACTGACATGATCTTTGATGAGATGTCAAGA	326
QY	301	GACTGGTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTTATGATGATGAGATGGAC	360
DB	327	GACTGGTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTTATGATGATGAGATGGAC	386
QY	361	CAGCAATCATGTGATAAGAAACATCATCTTAAAGCAAACTTTAGTGTGATTTTCGAAAGG	420
DB	387	CAGCAATCATGTGATAAGAAACATCATCTTAAAGCAAACTTTAGTGTGATTTTCGAAAGG	446
QY	421	CTGGAGACACTAATCTACTTACGACCTTCCAGGAGAGGAGCAGTCTGTTGGCGAAATT	480
DB	447	CTGGAGACACTAATCTACTTACGACCTTCCAGGAGAGGAGCAGTCTGTTGGCGAAATT	506
QY	481	TCACCATTCGCTTCTCTTCCAGGACATCTAATGAGATGTCAAAATGCAATTGGGGTC	540
DB	507	TCACCATTCGCTTCTCTTCCAGGACATCTAATGAGATGTCAAAATGCAATTGGGGTC	566
QY	541	CTCATTCGAGGACCTTAAATGGAAATGATACGTTAGAACTCTGAACTCTACAGAGA	600
DB	567	CTCATTCGAGGACCTTAAATGGAAATGATACGTTAGAACTCTGAACTCTACAGAGA	626
QY	601	TTCCGTTGGAGAGCAGTCTAGAAATGGGAGACCTTCAATCCCTCCAAAGCAGAAACGA	660
DB	627	TTCCGTTGGAGAGCAGTCTAGAAATGGGAGACCTTCAATCCCTCCAAAGCAGAAACGA	686
QY	661	AAATGGAGAGAACTTGGCCGAGAGTT	690
DB	687	AAATGGAGAGAACTTGGCCGAGAGTT	716

RESULT 10
 US-10-065-133A-50
 ; Sequence 50, Application US/10065133A
 ; Patent No. 6685946
 ; GENERAL INFORMATION:

; APPLICANT: Dowling, Patricia W.
 ; APPLICANT: Youngner, Julius S.
 ; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
 ; FILE REFERENCE: EQ-1-C2-1
 ; CURRENT APPLICATION NUMBER: US/10/065,133A
 ; CURRENT FILING DATE: 2002-12-10
 ; PRIOR APPLICATION NUMBER: PCT/US99/18583
 ; PRIOR FILING DATE: 1999-08-12
 ; PRIOR APPLICATION NUMBER: 09/133,921
 ; PRIOR FILING DATE: 1998-08-13
 ; NUMBER OF SEQ ID NOS: 108
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 50
 ; LENGTH: 891
 ; TYPE: DNA
 ; ORGANISM: Equine influenza virus H3N8
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (27)..(716)
 ; OTHER INFORMATION:
 ; US-10-065-133A-50

Query Match 100.0%; Score 690; DB 3; Length 891;
 Best Local Similarity 100.0%; Pred. No. 1.9e-212; Indels 0; Gaps 0;
 Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGGATTCCAACTGTGTCAAGCTTTCAGGTAGACTGTTTCTTTGGCATGTCCGCAAA	60
DB	27	ATGGATTCCAACTGTGTCAAGCTTTCAGGTAGACTGTTTCTTTGGCATGTCCGCAAA	86
QY	61	CGATTTCGACGACCAAGAACTGGGTGATGCCCATTCCTTGACCGGCTTCGCCGAGACG	120
DB	87	CGATTTCGACGACCAAGAACTGGGTGATGCCCATTCCTTGACCGGCTTCGCCGAGACG	146
QY	121	AAGTCCCTTAAAGAGAGAGTGTGATGCTTGGTCTGGACATCGAACAAGCCACTCGTGCA	180
DB	147	AAGTCCCTTAAAGAGAGAGTGTGATGCTTGGTCTGGACATCGAACAAGCCACTCGTGCA	206
QY	181	GGAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGGCACCTTAAATGACC	240
DB	207	GGAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGGCACCTTAAATGACC	266
QY	241	ATTGCTCTGTTCTCTGCTTACGCTACTTAACTGACATGATCTTTGATGAGATGTCAAGA	300
DB	267	ATTGCTCTGTTCTCTGCTTACGCTACTTAACTGACATGATCTTTGATGAGATGTCAAGA	326
QY	301	GACTGGTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTTATGATGATGAGATGGAC	360
DB	327	GACTGGTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTTATGATGATGAGATGGAC	386
QY	361	CAGCAATCATGTGATAAGAAACATCATCTTAAAGCAAACTTTAGTGTGATTTTCGAAAGG	420
DB	387	CAGCAATCATGTGATAAGAAACATCATCTTAAAGCAAACTTTAGTGTGATTTTCGAAAGG	446
QY	421	CTGGAGACACTAATCTACTTACGACCTTCCAGGAGAGGAGCAGTCTGTTGGCGAAATT	480
DB	447	CTGGAGACACTAATCTACTTACGACCTTCCAGGAGAGGAGCAGTCTGTTGGCGAAATT	506
QY	481	TCACCATTCGCTTCTCTTCCAGGACATCTAATGAGATGTCAAAATGCAATTGGGGTC	540
DB	507	TCACCATTCGCTTCTCTTCCAGGACATCTAATGAGATGTCAAAATGCAATTGGGGTC	566
QY	541	CTCATTCGAGGACCTTAAATGGAAATGATACGTTAGAACTCTGAACTCTACAGAGA	600
DB	567	CTCATTCGAGGACCTTAAATGGAAATGATACGTTAGAACTCTGAACTCTACAGAGA	626
QY	601	TTCCGTTGGAGAGCAGTCTAGAAATGGGAGACCTTCAATCCCTCCAAAGCAGAAACGA	660
DB	627	TTCCGTTGGAGAGCAGTCTAGAAATGGGAGACCTTCAATCCCTCCAAAGCAGAAACGA	686
QY	661	AAATGGAGAGAACTTGGCCGAGAGTT	690
DB	687	AAATGGAGAGAACTTGGCCGAGAGTT	716

RESULT 11
US-10-204-664A-6
; Sequence 6, Application US/10204664A
; Patent No. 6800288
; GENERAL INFORMATION:
; APPLICANT: FERKO, Boris
; APPLICANT: EGOROV, Andre
; APPLICANT: VOGLAUER, Regina
; TITLE OF INVENTION: Recombinant Influenza A Viruses
; FILE REFERENCE: 113529
; CURRENT APPLICATION NUMBER: US/10/204,664A
; PRIOR FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: EP 00104338.9
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 6
; LENGTH: 906
; TYPE: DNA
; ORGANISM: Influenza A virus /PRNS38
US-10-204-664A-6
Query Match 77.2%; Score 532.4; DB 3; Length 906;
Best Local Similarity 87.0%; Pred. No. 1.6e-161;
Matches 614; Conservative 0; Mismatches 76; Indels 16; Gaps 2;
QY 1 ATGGATTCCAAACACATGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCCGAAA 60
Db 27 ATGGATCCAAACACATGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCCGAAA 86
QY 61 CGATTTCGAGACCAAGAACTGGGTGATGCCCATTTCTTGACCGGCTTCGCCGAG----- 115
Db 87 CGATTTCGAGACCAAGAACTAGGTGATGCCCATTTCTTGATCGGCTTCGCCGAGTGAAT 146
QY 116 -----ACCAGAAGTCCCTAAAGAGAGAGTGTAGCACTCTTGCTTGGACATCGAA 165
Db 147 AACTAGCTGAATCAGAAATCCCTAAGAGAGAGGGGACACCCCTCGGTCTGCACATCGAG 206
QY 166 ACAGCCACTCGTGCAGAGAAACAGATAGTGGAGAGATCTTGGAGAGAGAGAGAGAGAG 225
Db 207 ACAGCCACAGTGTGGAGAGAGAGATAGTGGAGAGAGATCTTGGAGAGAGAGAGAGAG 266
QY 226 GCATTTAAATGACCAATGCTCTGTCTCTGCTTCAAGCTTCACTTAACTGACATGACTCTT 285
Db 267 GCATTTAAATGACCAATGCTCTGTCTCTGCTTCAAGCTTCACTTAACTGACATGACTCTT 326
QY 286 GATGAGATGTCAGAGACTGTTTCATGCTCATGCGCAAGAGAGAGAGAGAGAGAGAGAGAG 345
Db 327 GAGGAAATGTCAGAGAGACTGTTTCATGCTCATGCGCAAGAGAGAGAGAGAGAGAGAGAG 386
QY 346 TGATTAAGATGAGACCGAGCAATCATGGA-TAAGAAATCATCACTTAAAGCAAACTTTAG 404
Db 387 TGATTAAGATGAGACCGAGCAATCATGGA-TAAGAAATCATCACTTAAAGCAAACTTTAG 446
QY 405 TGTGATTTTCGAAGGCTGGAGACACTTAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 464
Db 447 TGTGATTTTCGAAGGCTGGAGACACTTAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 506
QY 465 AGTCGTTGGCGAAATTTTCAACATTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 524
Db 507 AATGTTGGCGAAATTTTCAACATTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 566
QY 525 AAATGCAATTTGGGGTCTTCAATCGAGAGACTTAAATGGAATGATTAATGATGATGATGAT 584
Db 567 AAATGCAATTTGGGGTCTTCAATCGAGAGACTTAAATGGAATGATTAATGATGATGATGAT 626
QY 585 TGAACCTCTACAGAGATTTGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 644
Db 627 TGAACCTCTACAGAGATTTGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 686
QY 645 TCCAAAGCAGAAACGAAATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTT 690

Db 687 TCCAAACAGAAACGAGAAATGCGGAGAACTAGGTAGTCAGAAAGTT 732
RESULT 12
US-09-506-286B-56
; Sequence 56, Application US/09506286B
; Patent No. 6492414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; CURRENT FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 56
; LENGTH: 293
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
US-09-506-286B-56
Query Match 42.2%; Score 291.4; DB 3; Length 293;
Best Local Similarity 99.7%; Pred. No. 6.7e-84;
Matches 292; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 398 ACTTTAGTGTGATTTTCGAAAGCTGGAGACACTAACTACTTACAGAGCTTTCACCGAAG 457
Db 1 ACTTTAGTGTGATTTTCGAAAGCTGGAGACACTAACTACTTACAGAGCTTTCACCGAAG 60
QY 458 AAGGAGAGAGTGTGGGCAAAATTCACCAATTCGCTTTCAGAGACATCTAATGAGG 517
Db 61 AAGGAGAGAGTGTGGGCAAAATTCACCAATTCGCTTTCAGAGACATCTAATGAGG 120
QY 518 ATGTCAAAAGAGCAATTTGGGCTTCATCGAGAGACTTAAATGGAATGATTAATGAGGTA 577
Db 121 ATGTCAAAAGAGCAATTTGGGCTTCATCGAGAGACTTAAATGGAATGATTAATGAGGTA 180
QY 578 GAATCTCTGAAACTCTACAGAGATTCGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGCTT 637
Db 181 GAATCTCTGAAACTCTACAGAGATTCGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGCTT 240
QY 638 CATTCCTCTCCAAAGCAGAAACGAAATGGAGAGAGAGAGAGAGAGAGAGAGAGAGTT 690
Db 241 CATTCCTCTCCAAAGCAGAAACGAAATGGAGAGAGAGAGAGAGAGAGAGAGAGAGTT 293
RESULT 13
US-10-065-133A-56
; Sequence 56, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 56
; LENGTH: 293
; TYPE: DNA

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; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-54
Query Match      42.2%; Score 291.4; DB 3; Length 293;
Best Local Similarity 99.7%; Pred. No. 6.7e-84;
Matches 292; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 398 ACTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATACTACTTAGAGCCTTCACCGAAG 457
Db 1 ACTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATACTACTTAGAGCCTTCACCGAAG 60

Qy 458 AAGGAGCAGTGGTGGGCAATTTACCAATTCGCTTCTTCAGGACATATAATGAGG 517
Db 61 AAGGAGCAGTGGTGGGCAATTTACCAATTCGCTTCTTCAGGACATATAATGAGG 120

Qy 518 ATGTCAAAAATGCAATTTGGGCTCTCATCGAGGACTTAAATGGAATGATAATACGGTTA 577
Db 121 ATGTCAAAAATGCAATTTGGGCTCTCATCGAGGACTTAAATGGAATGATAATACGGTTA 180

Qy 578 GAATCTCTGAAACTCTACAGAGATTCGCTTGGAGAGCAGTCATGAGATGGAGACCTT 637
Db 181 GAATCTCTGAAACTCTACAGAGATTCGCTTGGAGAGCAGTCATGAGATGGAGACCTT 240

Qy 638 CATTCCCTCCAAAGCAGAAACGAAATTCGAGAGACAAATTCGAGCAAGTT 690
Db 241 CATTCCCTCCAAAGCAGAAACGAAATTCGAGAGACAAATTCGAGCAAGTT 293

RESULT 14
US-09-506-286B-54
; Sequence 54, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; CURRENT FILING DATE: 2000-02-16
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(293)
US-09-506-286B-54

Query Match      42.2%; Score 291.4; DB 3; Length 468;
Best Local Similarity 99.7%; Pred. No. 8.6e-84;
Matches 292; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 398 ACTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATACTACTTAGAGCCTTCACCGAAG 457
Db 1 ACTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATACTACTTAGAGCCTTCACCGAAG 60

Qy 458 AAGGAGCAGTGGTGGGCAATTTACCAATTCGCTTCTTCAGGACATATAATGAGG 517
Db 61 AAGGAGCAGTGGTGGGCAATTTACCAATTCGCTTCTTCAGGACATATAATGAGG 120

Qy 518 ATGTCAAAAATGCAATTTGGGCTCTCATCGAGGACTTAAATGGAATGATAATACGGTTA 577
Db 121 ATGTCAAAAATGCAATTTGGGCTCTCATCGAGGACTTAAATGGAATGATAATACGGTTA 180

Qy 578 GAATCTCTGAAACTCTACAGAGATTCGCTTGGAGAGCAGTCATGAGATGGAGACCTT 637
Db 181 GAATCTCTGAAACTCTACAGAGATTCGCTTGGAGAGCAGTCATGAGATGGAGACCTT 240

Qy 638 CATTCCCTCCAAAGCAGAAACGAAATTCGAGAGACAAATTCGAGCAAGTT 690
Db 241 CATTCCCTCCAAAGCAGAAACGAAATTCGAGAGACAAATTCGAGCAAGTT 293

US-10-065-133A-54
; Sequence 54, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Equine influenza virus H3N8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(293)
; OTHER INFORMATION:
US-10-065-133A-54

Query Match      42.2%; Score 291.4; DB 3; Length 468;
Best Local Similarity 99.7%; Pred. No. 8.6e-84;
Matches 292; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 398 ACTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATACTACTTAGAGCCTTCACCGAAG 457
Db 1 ACTTTAGTGTGATTTTCGAAAGGCTGGAGACACTAATACTACTTAGAGCCTTCACCGAAG 60

Qy 458 AAGGAGCAGTGGTGGGCAATTTACCAATTCGCTTCTTCAGGACATATAATGAGG 517
Db 61 AAGGAGCAGTGGTGGGCAATTTACCAATTCGCTTCTTCAGGACATATAATGAGG 120

Qy 518 ATGTCAAAAATGCAATTTGGGCTCTCATCGAGGACTTAAATGGAATGATAATACGGTTA 577
Db 121 ATGTCAAAAATGCAATTTGGGCTCTCATCGAGGACTTAAATGGAATGATAATACGGTTA 180

Qy 578 GAATCTCTGAAACTCTACAGAGATTCGCTTGGAGAGCAGTCATGAGATGGAGACCTT 637
Db 181 GAATCTCTGAAACTCTACAGAGATTCGCTTGGAGAGCAGTCATGAGATGGAGACCTT 240

Qy 638 CATTCCCTCCAAAGCAGAAACGAAATTCGAGAGACAAATTCGAGCAAGTT 690
Db 241 CATTCCCTCCAAAGCAGAAACGAAATTCGAGAGACAAATTCGAGCAAGTT 293

Search completed: March 7, 2006, 22:51:36
Job time : 231.875 secs
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 00:06:39 : Search time 3487.17 Seconds
(without alignments)
9257.682 Million cell updates/sec

Title: US-10-734-373-59

Perfect score: 690

Sequence: 1 atggtatcccaactgtgtc.....gaacaattgagccagaagtt 690

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_hic.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_est7.*
9: gb_gsal.*
10: gb_gsal.*
11: gb_gsal.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	6.4	509	3	BM952076
2	40.8	5.9	544	3	BI885258
3	40.6	5.9	763	2	BE785748
4	40.4	5.9	474	9	AQ308098
5	40.4	5.9	593	7	CK336719
6	39.2	5.7	789	3	BI434619
7	38.4	5.6	981	10	CNS0064P
8	38	5.5	645	2	BE436394
9	38	5.5	689	2	BE436400
10	38	5.5	703	1	AJ784580
11	38	5.5	718	1	AJ831883
12	38	5.5	720	3	BM534953
13	38	5.5	724	2	BGI29051
14	38	5.5	775	7	CV470467
15	38	5.5	777	3	BM413146
16	38	5.5	799	3	BM535551
17	38	5.5	865	8	DN222619
18	37.8	5.5	484	3	BP883758
19	37.8	5.5	553	3	BM863758
20	37.8	5.5	745	1	AW037484
21	37.8	5.5	885	10	CG789515
22	37.6	5.4	1101	10	CNS0021J

23	37.6	5.4	1101	10	CNS00KK2
24	37.2	5.4	767	9	AZ242813
25	37.2	5.4	1185	6	CA462358
26	37	5.4	580	10	CL929673
27	37	5.4	824	6	CB634856
28	36.8	5.3	775	10	BI187584
29	36.8	5.3	985	10	CNS02K3U
30	36.6	5.3	485	2	BF711497
31	36.6	5.3	799	10	DU039001
32	36.4	5.3	505	9	AZ173148
33	36.4	5.3	635	3	BM360828
34	36.4	5.3	665	1	AW218935
35	36.2	5.2	384	7	CO497058
36	36.2	5.2	587	8	DN756261
37	36.2	5.2	725	10	CZ421104
38	36.2	5.2	744	5	BM716173
39	36.2	5.2	845	7	CO040945
40	36.2	5.2	848	7	CO02083
41	36.2	5.2	870	10	CG847516
42	36.2	5.2	871	7	CO125308
43	36.2	5.2	882	7	CO099059
44	36.2	5.2	900	7	CO124880
45	36.2	5.2	916	10	CG848245

ALIGNMENTS

RESULT 1
BM952076
LOCUS
DEFINITION rc55a04.y1 Meloidogyne hapla egg pAMP1 v1 Meloidogyne hapla cDNA 5' similar to SW:YXV4 CAEEL P34567 HYPOTHETICAL 67.2 KD PROTEIN T16H12.4 IN CHROMOSOME III. ; mRNA sequence.

ACCESSION BM952076
VERSION BM952076.1
KEYWORDS EST
SOURCE Meloidogyne hapla

ORGANISM Meloidogyne hapla
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Meloidogynidae; Meloidogyninae; Meloidogyne.

REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. DNA Sequencing by: Washington University Genome Sequencing Center
Seq primer: -40BP from Gibco
High quality sequence stop: 400.

FEATURES
source

1..509
/organism="Meloidogyne hapla"
/mol_type="mRNA"
/db_xref="taxon:6305"
/dev_stage="parasitic adult females"
/lab_host="DH10B"
/clone_lib="Meloidogyne hapla egg pAMP1 v1"
/note="Vector: pAMP1 (Gibco); Site 1: NotI; Site 2: SalI;
The library was constructed by Claire Murphy and Dr. James

/notes="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: oligo dt. Average insert size 1.8 kb. Library constructed by Life Technologies."

ORIGIN

Query Match 5.9%; Score 40.6; DB 2; Length 763;
Best Local Similarity 52.0%; Pred. No. 1.8;
Matches 91; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 290 AGATGTCACAGAGACTGGTTTCATGCTCATGCCCAAGCAGAAAGTACAGGCTCCCTATGTA 349
DB 392 AGCTGTCAATATAATATAATATGCTTTCTTAAAAAAGTATTTTACAGACAGATAGTGA 333

QY 350 TAAGATGACAGGCAATCATGATAGAACATCATCTTAAAGCAAACTTTAGTGTA 409
DB 332 TATACATTGTTGATGCTGGGCAAAAGAAAGCTAACACAAAGCTTAAGTGTA 273

QY 410 TTTTCGAAAGCTGGAGACACTAATCTACTTAGAGCCTTCACCGAAGAGGAC 464
DB 272 TATATTAAGATGATACATAATGACGTTTAAACCTGCATAGAATGAGC 218

RESULT 4

LOCUS AQ308098 474 bp DNA linear GSS 22-DEC-1998
DEFINITION C17B1-E1-2525L17.TP C17B1-E1 Homo sapiens genomic clone 2525L17,
genomic survey sequence.
ACCESSION AQ308098
VERSION AQ308098.1 GI:4040450
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Adams M.D., Rounalev, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
BERRY, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
Venter, J.C.
TITLE Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
JOURNAL Unpublished (1998)
COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hwe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

FEATURES

source
1. 474
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="2525L17"
/sex="male"
/cell_type="sperm"
/clone_lib="C17B1-E1"
/notes="Vector: pBelobAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"

ORIGIN

Query Match 5.9%; Score 40.4; DB 9; Length 474;
Best Local Similarity 58.2%; Pred. No. 1.8;
Matches 71; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 506 ATACTATGAGGTGTCAAAATGCAATGGGTCTCTCATCGGAGGACTTAATGGAATG 565

DB 142 ATACGATAGATCAAGTAAAAATGCAATTTGACATCTTCAACAGAAAGATTTGATCAACAG 201
QY 566 ATAAATACGGTTAGAACTCTGAAACTCTACAGAGATTGGCTTGGAGAACGACTCATGAGA 625
DB 202 AAGAAAGAAATCAGGCTATTTGAAATGCAAGAGAGAGAAAAAGAAAGCAACACGAGA 261
QY 626 AT 627
DB 262 AT 263

RESULT 5

LOCUS CK336719/c 593 bp mRNA linear EST 22-DEC-2003
DEFINITION C0254D07-3 NIA Mouse 7.5-dpc Whole Embryo cDNA Library (Long) Mus
musculus cDNA clone NIA:C0254D07 IMAGE:30015786 3', mRNA sequence.
ACCESSION CK336719
VERSION CK336719.1 GI:40292332
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1. (bases 1 to 593)
Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA libraries from
submicrogram amounts of total RNAs by a universal PCR amplification
method
Genome Res. 11 (9), 1553-1558 (2001)
11544199
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@gsun.grc.nia.nih.gov
Phone: 410-552-1000
Seq primer: -21M13 Forward
High quality sequence stop: 593
POLYA=yes

FEATURES

source
1. 593
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="nia:EST:C0254D07-3"
/db_xref="taxon:10090"
/clone="NIA:C0254D07 IMAGE:30015786"
/tissue_type="whole embryo including extraembryonic
tissues at 7.5-days postcoitum"
/dev_stage="7.5-days postcoitum"
/lab_host="DH10B"
/clone_lib="NIA Mouse 7.5-dpc Whole Embryo cDNA Library
(Long)"
/note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://gsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
extracted from a pool of four embryos at 7.5-days
postcoitum. Double-stranded cDNAs were synthesized with an
Oligo(dT) primer (Invitrogen):
5'-GGATCTCTAGTCAGCGCGCGCCCTCTTTTCTTTT-3' from
7 ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to lone-linker L1-SalI, purified by phenol/chloroform, and
separated from free linkers by Centrificon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex taq polymerase (Takara) with a primer SalI-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes

QY 287 ATGAGATGTCAAGAGACTGGTTTCATGCTCATGCCCAAGCAGAAAGTAAACAGCTCCCTAT 346
 Db 855 ATGTARCCCAAGAAATTTACTTTTATACATATATTAAGACACATARGAATTT 796
 QY 347 GTATAAGATGGACCGCAATCATGGATGAAGAACATCATCTTAAAGCAAACTTTAGTG 406
 Db 795 TGTAGGAGGGAATTTTAAAGATTAAAGAAAGAACTGTATGATATTAATAAATAAAG 736
 QY 407 TGATTTTCGAAGGCTGGAGACACTAATATCTTCTAGAGCTTACCGAAGAGGAGCAG 466
 Db 735 TAAATTTTAAATAATATAAATTTAAATTTAAGACTTCAAGATATTAATGAAGAGAGAAA 676
 QY 467 TCGTTGGCGAAATTTTCAACATTCCTCTCTCCAGACATATCAATGAGGATGTCAAA 526
 Db 675 AADVTGAAGAGCTTTCMAAGAAAMKTTCTTAGMTAAACCCCTATTGAGTATGTAAT 616
 QY 527 ATGCAATTTGGGCTTCATCGGAGGACTTAAATGGAATGATTAATACGGTTA 577
 Db 615 ATGTAATTTGMAAGGACCTACACTGAANAACCTGAATTTGACTTTGATNA 565

RESULT 8

BE436394/c
 LOCUS EST407472 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
 BE436394
 ACCESSION BE436394
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Lycopersicon esculentum (Solanum lycopersicum)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE
 AUTHORS 1 (bases 1 to 645)
 Alcalá, J., Vrebalov, J., White, R., van der Hoeven, R.S., Holt, I.E.,
 Liang, P., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronning, C.M.,
 Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and
 Tanksley, S.D.
 Generation of ESTs from tomato fruit tissue, breaker stage
 Contact: CGI
 Unpublished (2000)
 Clemson University
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 5 prime sequence.

FEATURES
 source
 Location/Qualifiers
 1..645
 /organism="Lycopersicon esculentum"
 /mol_type="mRNA"
 /cultivar="TA496"
 /db_xref="taxon:4081"
 /clone="cLEG32A24"
 /tissue_type="Pericarp"
 /dev_stage="breaker"
 /lab_host="SOLR"
 /clone_lib="tomato breaker fruit, TIGR"
 /notes="Vector: pBluescriptSKmCUadapt; Site 1: EcoRI;
 Site 2: XhoI; Fruit were harvested at the breaker stage
 (first sign of lycopene accumulation on the blossom end of
 the fruit). Fruit were cut in half and the seeds and
 locules were discarded prior to freezing the pericarp."

ORIGIN

Query Match 5.5%; Score 38; DB 2; Length 645;
 Best Local Similarity 60.8%; Pred. No. 10;
 Matches 62; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
 QY 144 CACTCTTGGTCTGGACATCGAAGCAGCACTCGTGCAGGAAAGCAGATATGAGCAGAT 203
 Db 411 CAGCCTAGTTTGACAAAGAAAGAACCCCATGCGGAGATATGATGATGAAGAA 352

ORIGIN

Query Match 5.5%; Score 38; DB 2; Length 645;
 Best Local Similarity 60.8%; Pred. No. 10;
 Matches 62; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
 QY 144 CACTCTTGGTCTGGACATCGAAGCAGCACTCGTGCAGGAAAGCAGATATGAGCAGAT 203
 Db 411 CAGCCTAGTTTGACAAAGAAAGAACCCCATGCGGAGATATGATGATGAAGAA 352

QY 204 TCTGGAAGAGGAATCAGATGAGGCACTTAAATGACCAATTCG 245
 Db 351 CATGTATGAGGACGCGTGTGAGGAATGAAGAAGCAATTCG 310

RESULT 9

BE436400
 LOCUS EST407478 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
 BE436400
 ACCESSION BE436400
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Lycopersicon esculentum (Solanum lycopersicum)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE
 AUTHORS 1 (bases 1 to 689)
 Alcalá, J., Vrebalov, J., White, R., van der Hoeven, R.S., Holt, I.E.,
 Liang, P., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronning, C.M.,
 Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and
 Tanksley, S.D.
 Generation of ESTs from tomato fruit tissue, breaker stage
 Contact: CGI
 Unpublished (2000)
 Clemson University
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 5 prime sequence.

FEATURES
 source
 Location/Qualifiers
 1..689
 /organism="Lycopersicon esculentum"
 /mol_type="mRNA"
 /cultivar="TA496"
 /db_xref="taxon:4081"
 /clone="cLEG32C12"
 /tissue_type="Pericarp"
 /dev_stage="breaker"
 /lab_host="SOLR"
 /clone_lib="tomato breaker fruit, TIGR"
 /notes="Vector: pBluescriptSKmCUadapt; Site 1: EcoRI;
 Site 2: XhoI; Fruit were harvested at the breaker stage
 (first sign of lycopene accumulation on the blossom end of
 the fruit). Fruit were cut in half and the seeds and
 locules were discarded prior to freezing the pericarp."

ORIGIN
 Query Match 5.5%; Score 38; DB 2; Length 689;
 Best Local Similarity 60.8%; Pred. No. 10;
 Matches 62; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
 QY 144 CACTCTTGGTCTGGACATCGAAGCAGCACTCGTGCAGGAAAGCAGATATGAGCAGAT 203
 Db 519 CAGCCTAGTTTGACAAAGAAAGAACCCCATGCGGAGATATGATGATGAAGAA 578

QY 204 TCTGGAAGAGGAATCAGATGAGGCACTTAAATGACCAATTCG 245
 Db 579 CATGTATGAGGACGCGTGTGAGGAATGAAGAAGCAATTCG 620

RESULT 10

BE436400
 LOCUS EST407478 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
 BE436400
 ACCESSION BE436400
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Lycopersicon esculentum (Solanum lycopersicum)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE
 AUTHORS 1 (bases 1 to 703)
 Alcalá, J., Vrebalov, J., White, R., van der Hoeven, R.S., Holt, I.E.,
 Liang, P., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronning, C.M.,
 Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and
 Tanksley, S.D.
 Generation of ESTs from tomato fruit tissue, breaker stage
 Contact: CGI
 Unpublished (2000)
 Clemson University
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 5 prime sequence.

FEATURES
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 Location/Qualifiers
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 /organism="Lycopersicon esculentum"
 /mol_type="mRNA"
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 /clone="cLEG32C12"
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 /dev_stage="breaker"
 /lab_host="SOLR"
 /clone_lib="tomato breaker fruit, TIGR"
 /notes="Vector: pBluescriptSKmCUadapt; Site 1: EcoRI;
 Site 2: XhoI; Fruit were harvested at the breaker stage
 (first sign of lycopene accumulation on the blossom end of
 the fruit). Fruit were cut in half and the seeds and
 locules were discarded prior to freezing the pericarp."

ORIGIN
 Query Match 5.5%; Score 38; DB 2; Length 703;
 Best Local Similarity 60.8%; Pred. No. 10;
 Matches 62; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
 QY 144 CACTCTTGGTCTGGACATCGAAGCAGCACTCGTGCAGGAAAGCAGATATGAGCAGAT 203
 Db 519 CAGCCTAGTTTGACAAAGAAAGAACCCCATGCGGAGATATGATGATGAAGAA 578

QY 204 TCTGGAAGAGGAATCAGATGAGGCACTTAAATGACCAATTCG 245
 Db 579 CATGTATGAGGACGCGTGTGAGGAATGAAGAAGCAATTCG 620

RESULT 10

BE436400
 LOCUS EST407478 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
 BE436400
 ACCESSION BE436400
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Lycopersicon esculentum (Solanum lycopersicum)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE
 AUTHORS 1 (bases 1 to 703)
 Alcalá, J., Vrebalov, J., White, R., van der Hoeven, R.S., Holt, I.E.,
 Liang, P., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronning, C.M.,
 Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and
 Tanksley, S.D.
 Generation of ESTs from tomato fruit tissue, breaker stage
 Contact: CGI
 Unpublished (2000)
 Clemson University
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 5 prime sequence.

FEATURES
 source
 Location/Qualifiers
 1..703
 /organism="Lycopersicon esculentum"
 /mol_type="mRNA"
 /cultivar="TA496"
 /db_xref="taxon:4081"
 /clone="cLEG32C12"
 /tissue_type="Pericarp"
 /dev_stage="breaker"
 /lab_host="SOLR"
 /clone_lib="tomato breaker fruit, TIGR"
 /notes="Vector: pBluescriptSKmCUadapt; Site 1: EcoRI;
 Site 2: XhoI; Fruit were harvested at the breaker stage
 (first sign of lycopene accumulation on the blossom end of
 the fruit). Fruit were cut in half and the seeds and
 locules were discarded prior to freezing the pericarp."

ORIGIN
 Query Match 5.5%; Score 38; DB 2; Length 703;
 Best Local Similarity 60.8%; Pred. No. 10;
 Matches 62; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
 QY 144 CACTCTTGGTCTGGACATCGAAGCAGCACTCGTGCAGGAAAGCAGATATGAGCAGAT 203
 Db 411 CAGCCTAGTTTGACAAAGAAAGAACCCCATGCGGAGATATGATGATGAAGAA 352

ORGANISM Lycopersicon esculentum var. cerasiforme
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 703)
Lemaire-Chamley, M., Petit, J., Garcia, V., Baldet, P., Pagard, M.,
Germain, V., Just, D. and Rothan, C.
Gene expression is spatially controlled in developing tomato fruit
Unpublished (2004)
Contact: Garcia V
Physiologie et Biotechnologie Vegetales
INRA
71 avenue E. Bourleaux, Villenave d'Ornon, 33883, FRANCE.
Location/Qualifiers
1..703
/organism="Lycopersicon esculentum var. cerasiforme"
/mol_type="mRNA"
/cultivar="West Virginia 106"
/db_xref="taxon:195583"
/clone="LE08CB07"
/tissue_type="fruit"
/dev_stage="8 days post anthesis"
/clone_lib="Lycopersicon esculentum var. cerasiforme fruit
8 days post anthesis"

ORIGIN
Query Match 5.5%; Score 38; DB 1; Length 703;
Best Local Similarity 60.8%; Pred. No. 10;
Matches 62; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 144 CACTCTTGCTGGACATCGAAACAGCCACTCGTCAGGAAAGCAGATAGTGAGCAGAT 203
|||
DB 282 CAAGCCTAGTTGGACAAAGAAAGACCCCATGCGAGGAATATGGATATGATGAAGA 341
|||

QY 204 TCTGGAAGAGGAATCAGATGAGGCACCTTAAATGACCAATTGC 245
|||
DB 342 CATGTATGAGGACGGTGTGAGGAATGAAGAACAATTGC 383
|||

RESULT 11
AJ831883/c
LOCUS
DEFINITION
AJ831883 Lycopersicon esculentum var. cerasiforme fruit 8 days post
anthesis Lycopersicon esculentum var. cerasiforme cDNA clone
LE08CB04, mRNA sequence.
AJ831883.1 GI:52619144
EST.
Lycopersicon esculentum var. cerasiforme (Solanum lycopersicum var.
cerasiforme)
ORGANISM
Lycopersicon esculentum var. cerasiforme
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 718)
Lemaire-Chamley, M., Petit, J., Garcia, V. and Rothan, C.
Transcriptional profiling of fruit tissues reveals novel features
of early fruit development in tomato
Unpublished (2004)
Contact: Garcia V
Physiologie et Biotechnologie Vegetales
INRA
71 avenue E. Bourleaux, Villenave d'Ornon, 33883, FRANCE.
Location/Qualifiers
1..718
/organism="Lycopersicon esculentum var. cerasiforme"
/mol_type="mRNA"
/cultivar="West Virginia 106"
/db_xref="taxon:195583"
/clone="LE08CB04"
/tissue_type="fruit"
/dev_stage="8 days post anthesis"
/clone_lib="Lycopersicon esculentum var. cerasiforme fruit
8 days post anthesis"

ORIGIN
Query Match 5.5%; Score 38; DB 1; Length 718;
Best Local Similarity 60.8%; Pred. No. 11;
Matches 62; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 144 CACTCTTGCTGGACATCGAAACAGCCACTCGTCAGGAAAGCAGATAGTGAGCAGAT 203
|||
DB 422 CAAGCCTAGTTGGACAAAGAAAGACCCCATGCGAGGAATATGGATATGATGAAGA 363
|||

QY 204 TCTGGAAGAGGAATCAGATGAGGCACCTTAAATGACCAATTGC 245
|||
DB 362 CATGTATGAGGACGGTGTGAGGAATGAAGAACAATTGC 321
|||

RESULT 12
BM534953/c
LOCUS
DEFINITION
BM534953
EST.
BM534953.1 GI:18813212
EST.
Lycopersicon esculentum (Solanum lycopersicum)
ORGANISM
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 720)
Alcala, J., Vrebalov, J., White, R., Vision, T., Karamycheva, S.A.,
Tsai, J., Bougri, O., Kirkness, E., Uterback, T., Van Aken, S.,
Ronning, C.M., Fraser, C.M., Martin, G.B., Fanksley, S.D. and
Giovannoni, J.
Generation of ESTs from tomato fruit tissue, breaker stage (2002)
Unpublished (2002)
Contact: CUGI
Clemson University
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
This clone is available through the Clemson University Genomics
Institute
Seq primer: T3.
Location/Qualifiers
1..720
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="CLEG64E13"
/tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
/clone_lib="tomato breaker fruit"
/notes="Vector: pBluescriptSKmCquadapt; Site 1: EcoRI;
Site 2: XhoI; supplier: Boyce Thompson Institute;
sequencing: The Institute for Genomic Research. Fruit
were harvested at the breaker stage (first sign of
lycopene accumulation on the blossom end of fruit). Fruit
were cut in half and the seeds and locules were discarded
prior to freezing the pericarp."

FEATURES
source
1..720

ORIGIN
Query Match 5.5%; Score 38; DB 3; Length 720;
Best Local Similarity 60.8%; Pred. No. 11;
Matches 62; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 144 CACTCTTGCTGGACATCGAAACAGCCACTCGTCAGGAAAGCAGATAGTGAGCAGAT 203
|||
DB 293 CAAGCCTAGTTGGACAAAGAAAGACCCCATGCGAGGAATATGGATATGATGAAGA 234
|||

QY 204 TCTGGAAGAGGAATCAGATGAGGCACCTTAAATGACCAATTGC 245
|||

[illegible]

Wed Mar 8 09:11:21 2006

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FEATURES
source
Location/Qualifiers
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/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="FM496"
/db_xref="taxon:4081"
/clones="cLEG2M4"
/tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
/clone_lib="tomato breaker fruit"
/note="Vector: pBluescriptSKmCladap; Site 1: EcoRI;
Site 2: XhoI; supplier: Boyce Thompson Institute;
sequencing: The Institute for Genomic Research. Fruit
were harvested at the breaker stage (first sign of
lycopene accumulation on the blossom end of fruit). Fruit
were cut in half and the seeds and locules were discarded
prior to freezing the pericarp."

ORIGIN
Query Match 5.5%; Score 38; DB 3; Length 777;
Best Local Similarity 60.8%; Pred. No. 11;
Matches 62; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 144 CACTCTTGCTGGACATCGAAACAGCCACTCGTCAGGAAAGCAGATAGTCGACGAT 203
DB 518 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 204 TCTGGAAGAGGAATCAGATGAGGCGCCTTAAATGACCATTCG 245
DB 578 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CATGTATGAGGACGGTGATGAGGAAATGAAGAAGACAATTGC 619
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Search completed: March 8, 2006, 04:47:27
Job time : 3491.17 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 7, 2006, 23:54:43 ; Search time 433.327 Seconds
(without alignments)
10612.397 Million cell updates/sec

Title: US-10-734-373-59

Perfect score: 690

Sequence: 1 atgtgattccacactgtgtc.....gaacaattgagccagaagtt 690

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_21.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	690	100.0	888	4 AAD15679	Aad15679 Equine in
2	690	100.0	888	4 AAD15681	Aad15681 Equine in
3	690	100.0	891	4 AAD15678	Aad15678 Equine in
4	682	98.8	693	2 AAT37435	Aat37435 Non-struct
5	590.8	85.6	1146	3 AAA75003	Aaa75003 Nucleotid
6	578	83.8	824	14 ADY62118	Ady62118 Influenza
7	573.2	83.1	824	14 ADY62117	Ady62117 Influenza
8	570	82.6	890	12 ADO15247	Ado15247 Influenza
9	568.4	82.4	890	2 AAX82197	Aax82197 Influenza
10	568.4	82.1	890	14 ADW44527	Adw44527 Influenza
11	566.8	82.1	890	6 AAD37061	Aad37061 Influenza
12	557.2	80.8	890	2 AAO22332	Aao22332 RNA (+)
13	539.6	78.2	890	6 ABA93942	Abag93942 Influenza
14	532.4	77.2	906	4 AAX77932	Aax77932 Nucleotid
15	291.4	42.2	468	4 AAD15680	Aad15680 Equine in
16	213.4	30.9	6010	2 AAX59676	Aat59676 Plasmid p
17	212.3	30.9	696	2 AAQ20237	Aaq20237 Encodes V
18	212.8	30.8	918	2 AAQ47361	Aaq47361 Sequence
19	212.8	30.8	918	2 AAQ70190	Aaq70190 Sequence

20	212.8	30.8	918	2 AAQ70208	Aaq70208 Sequence
21	212	30.7	453	2 AAT95097	Aat95097 Porcine s
22	212	30.7	453	6 AAD27035	Aad27035 Influenza
23	212	30.7	690	2 AAQ47362	Aaq47362 Sequence
24	212	30.7	690	2 AAQ70191	Aaq70191 Sequence
25	212	30.7	690	2 AAQ70209	Aaq70209 Sequence
26	212	30.7	924	2 AAQ04072	Aaq04072 Coding re
27	212	30.7	924	2 AAQ47364	Aaq47364 Sequence
28	212	30.7	924	2 AAQ70195	Aaq70195 Sequence
29	212	30.7	964	2 AAQ06580	Aaq06580 Plasmid s
30	212	30.7	1212	2 AAX87592	Aax87592 Haemagglu
31	211.6	30.7	681	2 AAQ47369	Aaq47369 Sequence
32	211.6	30.7	681	2 AAQ70201	Aaq70201 Sequence
33	211.6	30.7	717	2 AAQ47368	Aaq47368 Sequence
34	211.6	30.7	717	2 AAQ70200	Aaq70200 Sequence
35	211.6	30.7	729	2 AAQ04073	Aaq04073 Coding re
36	211.6	30.7	729	2 AAQ70197	Aaq70197 Sequence
37	211.4	30.6	912	2 AAQ70202	Aaq70202 Sequence
38	211.4	30.6	699	2 AAQ20236	Aaq20236 Encodes h
39	210.4	30.5	1014	2 AAO38091	Aao38091 NS1-19857
40	210.4	30.5	1017	2 AAO38093	Aao38093 NS1-ZS3 f
41	210.4	30.5	1017	2 AAO38092	Aao38092 NS1-ACAL
42	210.4	30.5	1020	2 AAO38090	Aao38090 NS1-ZQ1 f
43	210	30.4	729	2 AAQ47365	Aaq47365 Sequence
44	210	30.4	912	2 AAQ47370	Aaq47370 Sequence
45	209.2	30.3	849	6 AAT08209	Aat08209 Breast ca

ALIGNMENTS

RESULT 1

AAD15679

ID AAD15679 standard; DNA; 888 BP.

AC AAD15679;

XX

DT 15-NOV-2001 (first entry)

XX

DE Equine influenza virus H3N8 newt3NS888 DNA.

XX

KW Equine influenza virus; ei; cold adaptation; temperature sensitivity;

KW vaccine; newt3NS888 DNA; ds.

XX

OS Equine influenza virus H3N8.

XX

PN WO200160849-A2.

XX

PD 23-AUG-2001.

XX

PF 16-FEB-2001; 2001WO-US005048.

XX

PR 16-FEB-2000; 2000US-00506286.

XX

PA (UYPI-) UNIV PITTSBURGH.

XX

PI Dowling PW, Youngner JS;

 XX || DR | WPI; 2001-522584/57. |
XX	
PT	Novel isolated equine influenza virus (wild-type and cold-adapted) proteins and viruses containing nucleic acid molecules encoding the proteins, which are useful for protecting animals from influenza virus infections.
PT	
PT	Claim 2; Page 74; 172pp; English.
XX	
PS	The patent discloses cold-adapted equine influenza viruses and reasortant influenza A viruses comprising at least one genome segment of such an equine influenza virus, wherein the equine influenza virus genome segment confers at least one identifying phenotype of the cold-adapted equine influenza virus, such as cold adaptation, temperature sensitivity, dominant interference or attenuation. The viruses are useful for

CC protecting animals from diseases caused by influenza viruses. They are
 CC also used as vaccines. The present sequence is an equine influenza (ei)
 CC virus H3N8 neia23 (wild type) NS888 DNA

XX Sequence 888 BP; 298 A; 174 C; 198 G; 218 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 690; DB 4; Length 888;
 Best Local Similarity 100.0%; Pred. No. 1.1e-212;
 Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGATTCACACACGTGTCAGCTTTTCAGGTAGACCTTTCTTGGCATGTCCGCAA 60
 DB 25 ATGGATTCACACACGTGTCAGCTTTTCAGGTAGACCTTTCTTGGCATGTCCGCAA 84
 QY 61 CGATTTCAGACCAAGAACTGGGTGATGCCCATTTCTTGCACCGCTTCGCGAGACAG 120
 DB 85 CGATTTCAGACCAAGAACTGGGTGATGCCCATTTCTTGCACCGCTTCGCGAGACAG 144
 QY 121 AAGTCCCTAAAGGAAGAGGTAGACACTCTTGGTCTGACATCGAAACAGCCCTCTGTGCA 180
 DB 145 AAGTCCCTAAAGGAAGAGGTAGACACTCTTGGTCTGACATCGAAACAGCCCTCTGTGCA 204
 QY 181 GGAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGGCATTTAAATGACC 240
 DB 205 GGAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGGCATTTAAATGACC 264
 QY 241 ATTGCTCTGTTCTCTTACGCTACTTAACTGACATGACTCTTGTATGAGATGTCAGA 300
 DB 265 ATTGCTCTGTTCTCTTACGCTACTTAACTGACATGACTCTTGTATGAGATGTCAGA 324
 QY 301 GACTGGTTCATGCTCATGCTCCCAAGCAGAAAGTAACAGGCTCCCTATGTATAGATGGAC 360
 DB 325 GACTGGTTCATGCTCATGCTCCCAAGCAGAAAGTAACAGGCTCCCTATGTATAGATGGAC 384
 QY 361 CAGCAATCATGTAAGCAACATCATACTTAAAGCAAACTTTAGTGTGATTTTCCAAAGG 420
 DB 385 CAGCAATCATGTAAGCAACATCATACTTAAAGCAAACTTTAGTGTGATTTTCCAAAGG 444
 QY 421 CTGAGACACTTAATCTACTTACTAGAGCTTCACCGAAGAGGAGCAGTCTGTGCGCAATT 480
 DB 445 CTGAGACACTTAATCTACTTACTAGAGCTTCACCGAAGAGGAGCAGTCTGTGCGCAATT 504
 QY 481 TCACATTCCTCTCTCCAGGACATCTATGAGGATGTCAAAATGCAATTGGGGTC 540
 DB 505 TCACATTCCTCTCTCCAGGACATCTATGAGGATGTCAAAATGCAATTGGGGTC 564
 QY 541 CTGATCGGAGACTTAATGGAATGATATACGGTTAGAACTCTGAACTCTACAGAGA 600
 DB 565 CTGATCGGAGACTTAATGGAATGATATACGGTTAGAACTCTGAACTCTACAGAGA 624
 QY 601 TTCGCTTGGGAAGCAGTCATGAGAAATGGAGACCTTCATTCCTCCCAAGCAGAAACGA 660
 DB 625 TTCGCTTGGGAAGCAGTCATGAGAAATGGAGACCTTCATTCCTCCCAAGCAGAAACGA 684
 QY 661 AAAATGGAGAGAACAAATTGAGCCAGAGTT 690
 DB 685 AAAATGGAGAGAACAAATTGAGCCAGAGTT 714

RESULT 2
 AAD15681
 ID AAD15681 standard; DNA; 888 BP.
 XX
 AC AAD15681;
 XX
 XX
 DT 15-NOV-2001 (first entry)
 XX
 DE Equine influenza virus H3N8 neia23 NS888 DNA.
 XX
 KW Equine influenza virus; ei; cold adaptation; temperature sensitivity;
 KW vaccine; neia23 NS888 DNA; Peia23 NS230 protein; ds.
 XX
 OS Equine influenza virus H3N8.

XX Key Location/Qualifiers
 FH 27. .719
 FT /tag= a
 FT /product= "Peia23 NS230 protein"
 FT 27. .716
 FT /tag= b
 FT /note= "This region is specifically claimed as SEQ ID NO:
 FT 41 in claim 2 of the specification"
 XX misc_feature
 XX WO200160849-A2.
 XX 23-AUG-2001.
 XX 16-FEB-2001; 2001WO-US005048.
 XX 16-FEB-2000; 2000US-00506286.
 XX (UYPI-) UNIV PITTSBURGH.
 XX Dowling PW, Youngner JS;
 XX P-PSDB; AAE09029.
 XX WPI; 2001-522584/57.
 XX Novel isolated equine influenza virus (wild-type and cold-adapted)
 XX proteins and viruses containing nucleic acid molecules encoding the
 XX proteins, which are useful for protecting animals from influenza virus
 XX infections.
 XX Claim 2; Page 75-76; 172pp; English.
 XX The patent discloses cold-adapted equine influenza viruses and
 XX reasortant influenza A viruses comprising at least one genome segment of
 XX such an equine influenza virus, wherein the equine influenza virus genome
 XX segment contains at least one identifying phenotype of the cold-adapted
 XX equine influenza virus, such as cold adaptation, temperature sensitivity,
 XX dominant interference or attenuation. The viruses are useful for
 XX protecting animals from diseases caused by influenza viruses. They are
 XX also used as vaccines. The present sequence is equine influenza (ei)
 XX virus H3N8 neia23 (cold adapted) NS888 DNA encoding Peia23 NS230 protein
 XX
 SQ Sequence 888 BP; 300 A; 173 C; 198 G; 217 T; 0 U; 0 Other;
 Query Match 100.0%; Score 690; DB 4; Length 888;
 Best Local Similarity 100.0%; Pred. No. 1.1e-212;
 Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGATTCACACACGTGTCAGCTTTTCAGGTAGACCTTTCTTGGCATGTCCGCAA 60
 DB 27 ATGGATTCACACACGTGTCAGCTTTTCAGGTAGACCTTTCTTGGCATGTCCGCAA 86
 QY 61 CGATTTCAGACCAAGAACTGGGTGATGCCCATTTCTTGCACCGCTTCGCGAGACAG 120
 DB 87 CGATTTCAGACCAAGAACTGGGTGATGCCCATTTCTTGCACCGCTTCGCGAGACAG 146
 QY 121 AAGTCCCTAAAGGAAGAGGTAGACACTCTTGGTCTGACATCGAAACAGCCCTCTGTGCA 180
 DB 147 AAGTCCCTAAAGGAAGAGGTAGACACTCTTGGTCTGACATCGAAACAGCCCTCTGTGCA 206
 QY 181 GGAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGGCATTTAAATGACC 240
 DB 207 GGAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGGCATTTAAATGACC 266
 QY 241 ATTGCTCTGTTCTCTTACGCTACTTAACTGACATGACTCTTGTATGAGATGTCAGA 300
 DB 267 ATTGCTCTGTTCTCTTACGCTACTTAACTGACATGACTCTTGTATGAGATGTCAGA 326
 QY 301 GACTGGTTCATGCTCATGCTCCCAAGCAGAAAGTAACAGGCTCCCTATGTATAGATGGAC 360
 DB 327 GACTGGTTCATGCTCATGCTCCCAAGCAGAAAGTAACAGGCTCCCTATGTATAGATGGAC 386
 QY 361 CAGGCAATCATGGAATAGAACATCATCTTAAAGCAAACTTTAGTGTGATTTTCGAAAGG 420

Db 387 CAGCAATCATGATGAAGAACATCATCTTAAAGCAAACTTTAGTGTGATTTTCGAAGG 446
 Qy 421 CTGGAGACCTAATCTACTTAGAGCCTTCCACGAAGAAGAGAGAGTCTGTTGGCGAAAT 480
 Db 447 CTGGAGACCTAATCTACTTAGAGCCTTCCACGAAGAAGAGAGAGTCTGTTGGCGAAAT 506
 Qy 481 TCACCATGCTCTCTCTCCAGGACATCTAATGAGATGTCAGAAATGCAATTTGGGGTC 540
 Db 507 TCACCATGCTCTCTCTCCAGGACATCTAATGAGATGTCAGAAATGCAATTTGGGGTC 566
 Qy 541 CTCATCGGAGACTTAAATGGAATGATAATACGTTTGAATCTCTGAACTCTACAGAGA 600
 Db 567 CTCATCGGAGACTTAAATGGAATGATAATACGTTTGAATCTCTGAACTCTACAGAGA 626
 Qy 601 TTCGCTTGGAGAGCAGTCATGAGATGGAGACCTTCATTTCCCTCCAGAGCAAGCA 660
 Db 627 TTCGCTTGGAGAGCAGTCATGAGATGGAGACCTTCATTTCCCTCCAGAGCAAGCA 686
 Qy 661 AAAATGGAGAGCAATTTGAGCCAGAGTT 690
 Db 687 AAAATGGAGAGCAATTTGAGCCAGAGTT 716

RESULT 3

AAD15678
 ID AAD15678 standard; DNA; 891 BP.

AC AAD15678;

XX 15-NOV-2001 (first entry)

DT Equine influenza virus H3N8 neiwt1NS891 DNA.

XX Equine influenza virus; ei; cold adaptation; temperature sensitivity;
 KW vaccine; neiwt1NS891 DNA; neiwt1NS230 protein; ds.

XX Equine influenza virus H3N8.

PH Key Location/Qualifiers

FT CDS 27..719

FT /tag= a

FT /product= "Peiwt1NS230 protein"

FT 27..716

FT /tag= b

FT /notes= "This region specifically claimed as SEQ ID NO: 34

FT in claim 2 of the specification"

XX WO200160849-A2.

XX 23-AUG-2001.

XX 16-FEB-2001; 2001WO-US005048.
 PF

XX 16-FEB-2000; 2000US-00506286.
 PR

XX (UYP1-) UNIV PITTSBURGH.

XX Dowling PW, Youngner JS;

XX WPI; 2001-522584/57.

XX P-PSDB; AAE09027.

XX Novel isolated equine influenza virus (wild-type and cold-adapted)
 PT proteins and viruses containing nucleic acid molecules encoding the
 PT proteins, which are useful for protecting animals from influenza virus
 PT infections.

XX Claim 2; Page 71-72; 172pp; English.
 DS

XX The patent discloses cold-adapted equine influenza viruses and
 CC reasortant influenza A viruses comprising at least one genome segment of
 DE such an equine influenza virus, wherein the equine influenza virus genome
 CC

CC segment confers at least one identifying phenotype of the cold-adapted
 CC equine influenza virus, such as cold adaptation, temperature sensitivity,
 CC dominant interference or attenuation. The viruses are useful for
 CC protecting animals from diseases caused by influenza viruses. They are
 CC also used as vaccines. The present sequence is an equine influenza (ei)
 CC virus H3N8 neiwt1 (wild type) NS891 DNA encoding peiwt1NS230 protein
 XX

SQ Sequence 891 BP; 300 A; 174 C; 199 G; 218 T; 0 U; 0 Other;

Query Match 100.0%; Score 690; DB 4; Length 891;

Best Local Similarity 100.0%; Pred. No. 1.le-212;

Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGATTCACACCTGTGTCAAGCTTCAGGTAGACACTGTTCTTGGCATGTCCGAAA 60

Db 27 ATGGATTCACACCTGTGTCAAGCTTCAGGTAGACACTGTTCTTGGCATGTCCGAAA 86

Qy 61 CGATTTCGAGACCAAGAACTGGGTGATGCCCCATTCCTGACCGGCTTCGCCGAGACAG 120

Db 87 CGATTTCGAGACCAAGAACTGGGTGATGCCCCATTCCTGACCGGCTTCGCCGAGACAG 146

Qy 121 AAGTCCCTAAAAGGAGAGGTAGCACTCTTGGTCTGACATCGAATCGAAACAGCCACTCGTGA 180

Db 147 AAGTCCCTAAAAGGAGAGGTAGCACTCTTGGTCTGACATCGAATCGAAACAGCCACTCGTGA 206

Qy 181 GGAAAGCAGATAGTGGAGCAGAACTTCGGAAGAGGAATCAGATGAGGACCTTAAATGACC 240

Db 207 GGAAAGCAGATAGTGGAGCAGAACTTCGGAAGAGGAATCAGATGAGGACCTTAAATGACC 266

Qy 241 ATTGGCTCTGTTCTCTGCTTCAGCGTACTTAACTGACATGACTCTTGTATGAGATGTCAAGA 300

Db 267 ATTGGCTCTGTTCTCTGCTTCAGCGTACTTAACTGACATGACTCTTGTATGAGATGTCAAGA 326

Qy 301 GACTGTTTCATGCTCATGCCAAGCAGAAAGTAAACAGCTCCCTATGTATAGATGTGAC 360

Db 327 GACTGTTTCATGCTCATGCCAAGCAGAAAGTAAACAGCTCCCTATGTATAGATGTGAC 386

Qy 361 CAGGCANTCATGTATAGACATCATCTTAAAGCAAACTTTAGTGTGATTTTCGAAGG 420

Db 387 CAGGCANTCATGTATAGACATCATCTTAAAGCAAACTTTAGTGTGATTTTCGAAGG 446

Qy 421 CTGGAGACACTAATCTACTTAGAGCCTTCACGAAGAGAGAGAGAGAGAGAGAGAGAGAG 480

Db 447 CTGGAGACACTAATCTACTTAGAGCCTTCACGAAGAGAGAGAGAGAGAGAGAGAGAGAG 506

Qy 481 TCACCATGCTCTCTCTTCCAGGACATCTAATGAGATGTCAAAATGCAATTTGGGGTC 540

Db 507 TCACCATGCTCTCTCTTCCAGGACATCTAATGAGATGTCAAAATGCAATTTGGGGTC 566

Qy 541 CTCATCGGAGACTTAAATGGAATGATAATACGTTTGAATCTCTGAAATCTACAGAGA 600

Db 567 CTCATCGGAGACTTAAATGGAATGATAATACGTTTGAATCTCTGAAATCTACAGAGA 626

Qy 601 TTCGCTTGGAGAGCAGTCATGAGATGGAGACCTTCATTTCCCTCCAAAGCAGAAACGA 660

Db 627 TTCGCTTGGAGAGCAGTCATGAGATGGAGACCTTCATTTCCCTCCAAAGCAGAAACGA 686

Qy 661 AAAATGGAGAGCAATTTGAGCCAGAGTT 690

Db 687 AAAATGGAGAGCAATTTGAGCCAGAGTT 716

RESULT 4

NAT37435

ID AAT37435 standard; DNA; 693 BP.

XX AC AAT37435;

XX 16-OCT-2003 (revised)

DT 09-APR-1997 (first entry)

XX Non-structural protein NS1 of influenza A virus.
 DE
 XX

KW Non-structural protein; NS1; influenza virus; respiratory tract;
KW diagnosis; anti-NS1 antibody; primer; PCR; detection; amplify; ss.
XX
OS Influenza virus; A/equine 1/Suffolk 89.
XX
XX EP726316-A2.
XX
XX 14-AUG-1996.
XX
XX 31-JAN-1996; 96EP-00300681.
XX
XX 09-FEB-1995; 95GB-00002489.
XX
XX (ANIM-) ANIMAL HEALTH TRUST.
XX
XX Binns M, Birch-Wachin I;
XX
XX WPI; 1996-364394/37.
XX
XX P-PSDB; AAW03522.
XX
XX Recombinant equine influenza virus NS1 protein - useful for diagnosis of
XX equine influenza A.
XX
XX Claim 1; Fig 1A; 20pp; English.
XX
XX This sequence encodes non-structural protein NS1 of influenza virus
XX A/equine 2/Suffolk 89. The NS1 protein is useful for diagnosis of equine
XX influenza A infections by detection of anti-NS1 antibodies. The NS1
XX coding sequence was isolated using the primer sequences given in AAT37436
XX -40. (Updated on 16-OCT-2003 to standardise OS field)
XX
XX Sequence 693 BP; 215 A; 146 C; 166 G; 166 T; 0 U; 0 Other;

Query Match 98.8%; Score 682; DB 2; Length 693;
Best Local Similarity 99.3%; Pred. No. 3.8e-210;
Matches 685; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1 ATGGATTCCAACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCGCAAA 60
DB 1 ATGGATTCCAACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCGCAAA 60
OY 61 CGATTTCGAGACCAAGAACTGGGTGATGCCCATTCCTTCACCGGCTTCGCCGAGACAG 120
DB 61 CGATTTCGAGACCAAGAACTGGGTGATGCCCATTCCTTCACCGGCTTCGCCGAGACAG 120
OY 121 AAGTCCCTAAAAGGAAGAGGTAGCTCTTGTCTGGACATCGAAGCCACTCGTGCA 180
DB 121 AAGTCCCTAAAAGGAAGAGGTAGCTCTTGTCTGGACATCGAAGCCACTCGTGCA 180
OY 181 GGAAGCGATAGTGGAGCAGATTCGGAAGGGAATCAGATCAGGCACTTAAATGACC 240
DB 181 GGAAGCGATAGTGGAGCAGATTCGGAAGGGAATCAGATCAGGCACTTAAATGACC 240
OY 241 ATGGCTCTGTCTCGCTTCAAGCTTAACTGACATGACTCTTGATGAGATGTCAAGA 300
DB 241 ATGGCTCTGTCTCGCTTCAAGCTTAACTGACATGACTCTTGATGAGATGTCAAGA 300
OY 301 GACTGGTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTATGTATAGATGAC 360
DB 301 GACTGGTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTATGTATAGATGAC 360
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DB 361 CAGGCAATCATGGATAGAAACATCATCTACTTAAAGCAAACTTTAGTGTGATTTTCAAGG 420
OY 421 CTGGAGACACTAATCTACTTAGAGCTTTTCACCGAAGGAGCAGCTCGTTGGCGAAATT 480
DB 421 CTGGAGACACTAATCTACTTAGAGCTTTTCACCGAAGGAGCAGCTCGTTGGCGAAATT 480
OY 481 TCACCAATTCGCTTCTCTTCCAGGACATCTAATGAGGATGTCAAAATGCAATTTGGGGTC 540
DB 481 TCACCAATTCGCTTCTCTTCCAGGACATCTAATGAGGATGTCAAAATGCAATTTGGGGTC 540

OY 541 CTCATCGGAGACTTAATGAATGATAATAACGGTTAGAACTCTGAAACTCTACAGAGA 600
DB 541 CTCATCGGAGACTTAATGAATGATAATAACGGTTAGAACTCTGAAACTCTACAGAGA 600
OY 601 TTGCTTTGGAGAGCAGTCATGAGAATGGGAGACCTTCATTCCCTCCAAAGCAGAAACGA 660
DB 601 TTGCTTTGGAGAGCAGTCATGAGAATGGGAGACCTTCATTCCCTCCAAAGCAGAAACGA 660
OY 661 AAAATGGAGAGCAAAATTGAGCAGAAATT 690
DB 661 AAAATGGAGAGCAAAATTGAGCAGAAATT 690

RESULT 5

AAAY5003/c

ID AAAY5003 standard; DNA; 1146 BP.

XX

AC AAAY5003;

XX

DT 02-JAN-2001 (first entry)

XX

DE Nucleotide sequence of an Influenza virus polynucleotide.

XX

KW Recombinant virus; vaccine; infection; hepatitis C virus vaccine;
KW human immunodeficiency virus vaccine; HIV vaccine; tumour vaccine; ss.

XX

OS Influenza virus.

XX

PN EP1035209-A1.

XX

XX 13-SEP-2000.

XX

XX 06-MAR-1999; 99EP-00104519.

XX

XX 06-MAR-1999; 99EP-00104519.

XX

XX (ARTE-) ARTEMIS PHARM GMBH.

XX

XX Hobom G, Flick R, Menke A, Azzey M;

XX

XX WPI; 2000-559876/52.

XX

PT Recombinant influenza virus useful for gene therapy and as a vaccine
PT against influenza and other infections, comprises viral RNA molecule
PT exchanged for a viral RNA encoding foreign gene.

XX

XX Disclosure; Page 17-18; 49pp; English.

XX

CC The specification describes a recombinant influenza virus, which is
CC genetically stable in the absence of helper virus. The influenza virus
CC has at least one of the regular viral RNA segments exchanged for a viral
CC RNA encoding a foreign gene. The virus also has at least one of the
CC regular viral RNA segments in an ambisense RNA molecule containing one of
CC the standard viral genes in sense orientation and a foreign, recombinant
CC gene in anti-sense orientation, or vice versa. The recombinant viruses
CC are useful for preparing vaccines in the form of inactivated preparations
CC or live recombinant viruses which are protective against influenza and
CC against other infections. The viruses are also useful in somatic gene
CC therapy, for transfer and expression of foreign genes into cells infected
CC by such viruses. They are also useful for design and production of
CC hepatitis C virus, human immunodeficiency virus (HIV) and tumour
CC vaccines. The present sequence represents an influenza virus sequence
CC which is used to produce viruses of the invention

XX Sequence 1146 BP; 271 A; 287 C; 233 G; 355 T; 0 U; 0 Other;

XX

Query Match 85.6%; Score 590.8; DB 3; Length 1146;

XX

Best Local Similarity 91.0%; Pred. No. 1.9e-180;

XX

Matches 628; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

XX

OY 1 ATGATTTCCAACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCGCAAA 60

DB 1024 ATGATTTCCAACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCGCAAA 965

Qy	61	CGATTTCGAGACCAAGAACTCTGGTGTGATGCCCAATCCCTTGACGGCTTCGCGGACGAG	120
Db	964	CGATTTCGAGACCAAGAAATGGGTGATGCCCAATCCCTTGACCGACTTCGCCGAGATCAG	905
Qy	121	AAGTCCTCTAAAAGCAAGAGGTAGCACTCTTGGTCTGGACATCGAAACAGGCACATCTGGTGA	180
Db	904	AAGTCCTCTGAGGGAGAGCGACGACACTCTTGGTCTGGACATCGACACAGCTACTCTGGTGT	845
Qy	181	GGAAAGCAGATAGTGGAGCAGAGATCTGGAGAGAGAAATCAGATAGGCGACTTTAAATGAACC	240
Db	844	GGAAAGCAGATAGTGGAGCGGAAATCTGGAGGAGCAATCGATAGGCGACTTTAAATGAACC	785
Qy	241	ATTGCCCTCTGTCTCTGCTCTCAGCGCTACTTAACTTGACATGACTCTTGATGAGATGTCAAGA	300
Db	784	ATTGCCCTCTGTACTCTGCTACAGCTACTCTAACTTGACATGACTCTTGAGAGAGATGTCAAGG	725
Qy	301	GACTGGTTCATGCTCATGCCCAAGCAGAAAAGTAAACAGGCTCCCTATGTATAAGAAATGGAC	360
Db	724	GACTGGTTCATGCTCATGGCCAAAACAGAAAGTGGCAGGCTCCCTTTGCATCAGAAATGGAC	665
Qy	361	CAGGCAATCATGGATTAAGAAATCATCATCTTAAAGCAAACTTTAGTGTGATTTTCGAAAGG	420
Db	664	CAGGCGATCATGGGGAAGAACATCATCTGAAGACAACTTCAGTGTGATTTTCGATCGG	605
Qy	421	CTGGAGACACTAAATACTTACTTAGAGCCTTCAACGAGAGAGAGCGACGCTCGGTGGCGGAATTT	480
Db	604	CTGGAACTCTCATACTTTAAGGGCTTAAACGATAGGGGCAATTTCTGGCGGAATTT	545
Qy	481	TCACCATTTGCCCTCTCTCTCCGAGCACTACTAATGAGGATGTCAAAATGCATTTGGGGTTC	540
Db	544	TCACCATTTGCCCTCTCTTCAGGACACTACTGATGAGGATGTCAAAATGCATTTGGGGTTC	485
Qy	541	CTCATTCGAGGACTTAAATGGAAATGATATAACGGTTTAGAAATCTCTGAAATCTCTACAGAGA	600
Db	484	CTCATTCGAGGACTTGAATGGAAATGATAACACAGTTTCGAGTCTCTGAATCTATACAGAGA	425
Qy	601	TTCCGCTTCGGAGACGAGTCAATGAGAAATGGGAGACCTTCATTCCCTCCAAAGCAGAAACGA	660
Db	424	TTCCGCTTCGGAGACGAGTAAATGAGAAATGGGGGACCTTCCACTCCCTCCAAAGCAGAAACGG	365
Qy	661	AAATGGAGAGAACAAATTTGAGCCAGAAATT	690
Db	364	AAATGGGAGAGAACAAATTTGAGTCAGAAATTT	335

RESULT 6	
ADY62118	
ID	ADY62118 standard; DNA; 824 BP.
XX	
XX	
XX	ADY62118;
XX	
DT	19-MAY-2005 (first entry)
XX	
DE	Influenza A virus strain A/England/1/53v-a mutant NS1 gene for vaccine.
XX	
KW	protein engineering; immune stimulation; immunostimulant; vaccine;
KW	influenza virus infection; mutant; gene; ds.
XX	
XX	
OS	Influenza A virus; strain A/England/1/53v-a.

XX	US2005054846-A1.
PN	
XX	
XX	10-MAR-2005.
PD	
XX	
PF	04-SEP-2003; 2003US-00654737.
XX	
PR	04-SEP-2003; 2003US-00654737.

(WEBS/) WEBSTER R G.
PA (WEBB/) WEBBY R J.
BA (OZAKI/) OZAKI H.
XX

webster RG, Webby RJ, Ozaki H;
PI
XX
WPT; 2005-213104/22.
DR P-PDSB; ADY62121.
DR
XX
Producing a reassortant influenza virus that gives a high titer in Vero
PT cells (certified for use in vaccine-production), comprises replacing the
PT NS gene of the A/PuertoRico/3/724 master strain with the NS gene of the
PT A/England/1/53 strain.
XX
XX
Claim 8; SEQ ID NO 2; 16pp; English.
XX
The invention relates to a method of producing a high titer reassortant
CC influenza virus by transfecting host cells with expression plasmids
CC containing the PB2, PB1, PA, NP, and M genes from the A/PuertoRico/8/34
CC influenza strain, the NS gene from the A/England/1/53 influenza strain
CC and the HA and NA genes from an influenza virus of interest other than
CC A/England/1/53, to obtain a high titer reassortant influenza virus. The
CC method is useful for producing a high titer reassortant influenza virus.
CC The high titer reassortant influenza viruses are useful for producing
CC influenza viral infections. The vaccines are useful for treating or preventing
CC rapid production of custom made attenuated virus vaccines, but vaccine
CC use is limited by the need to use vaccine approved cell lines. The master
CC strain A/PuertoRico/8/34 which is the most widely used in producing
CC recombinant viruses for vaccine use produces a high titer in MDCK cells,
CC which are not certified for use in production of human vaccines, but not
CC in Vero cells, which are certified for this use. The applicants have
CC discovered that replacing the NS gene of the A/PuertoRico/3/724 master
CC strain with the NS gene of the A/England/1/53 strain gives reassortant
CC virus that produces a high titer in Vero cells. This sequence corresponds
CC to the coding sequence for the NS1 protein from the A/England/1/53v-a
CC influenza strain. This strain encodes the protein with the amino acid
CC changes Q21R/T58I/V60A/N127S/V174I/D199N/delta231-238.
XX
Sequence 824 BP; 263 A; 167 C; 203 G; 191 T; 0 U; 0 Other

QY	1	ATGGATTCCAAACACTGTGTCAAGCTTTTCAGSTAGACTGTTTCTTTTGGCATGTCCGCAAA	60
DB	6	ATGGATCCCAACACTGTGTCAAGCTTTTCAGSTAGATTGCTTTCTTTGGCATGTCCGCAAA	65
QY	61	CGATTTCAGACAAGAAACTGGGTGATGCCCCATTCCTTCGACCGGCTTCGCCGAGACGAG	120
DB	66	CGAGTTGCAGACAAGAACTAGGTGATGCCCCATTCCTTCGATCGGCTTCGCCGAGATCAG	125
QY	121	AAGTCCCTTAAAGGAAGAGAGTAGCACTCTTGTGCTGACACATCGAAACAGCAACTCGTGTGA	180
DB	126	AAGTCCCTTAAAGGAAGAGAGTAGCACTCTCGGGCTGAAACATCGAAACAGCCATCCGTGCT	185
QY	181	GGAAAGCAGATAGTGAGCAGATTTCTGGAGAGGAAGTCCAGATGAGCGACTTAAATAAGCC	240
DB	186	GGAAAGCAAAATAGTGAGCGGATTTCTGAAGGAAGAAATCCGATGAGCGACTTAAATAAGCC	245
QY	241	ATTGGCTCTGTTCCTGCTTCACGCTATTAACTGACATGACTCTTCGTAGAGATGTCGAAGA	300
DB	246	ATGGGCTCTGCGACTGCTTCGCGCTACTTAACTGACATGACTATTGAGSAATGTCGAAGG	305
QY	301	GACTGGTTTCATGCTCATGCCCCACAGCAAGTAAACAGGCTCCCTATGTATGAAGAAATGGAC	360
DB	306	GACTGGTTTCATGCTCATGCCCCACAGCAAGTTCGCGAGGCCCTCTTTGTATCAGAATGGAC	365
QY	361	CAGGCAATCATGATGAAGAAACATCACTTTAAAGCAAACTTTAGTGTGATTTTCGAAGG	420
DB	366	CAGGCGATCATGATGAAGAGCATCATACTGAAGCGCACTTCAGTGTGATTTTTCGACCG	425

QY	421	CTGGAGACCTAACTACTCTTAGAGCCTTCA	CCGAAGAAGGAGCAGCTCGTTGGCGAAATT	480
Db	426	CTGGAGACTCTAATATTACTTAAGGCGTTT	CCGAAGAGGGGAGCAATTTGTTGGCGAAATT	485
QY	481	TCACCAATTGCTTCTCTTCCAGGACATACTA	TATGAGGATGTCAAAATGCGAATTGGGGTCT	540
Db	486	TCACCAATTGCTTCTCTTCCAGGACATACTA	TATGAGGATGTCAAAATGCGAATTGGGGTCT	545
QY	541	CTCATCGGAGGACTTAATGGAATGATTAAT	CGGTAGACTCTCGAATCTACGACAGA	600
Db	546	CTCATCGGAGGACTTAATGGAATGATTAAT	CGAGTCTCTTAATCTCTACAGGA	605
QY	601	TTGCGTTGGAGAGCACTCATGAGAAATGGG	AGACCTTCACTCCCTCCAAAGCAGAAACGA	660
Db	606	TTGCGTTGGAGAGCACTCATGAGAAATGGG	AGACCTTCACTCCAAACAGAAACGG	665
QY	661	AAATTCGAGAGCACAATTGGAGCCAGAGTT		690
Db	666	AAATTCGAGAGCACAATTGGAGTCAGAGTT		695

RESULT 7	
AD62117	
ID	ADY62117 standard, DNA, 824 BP.
XX	
XX	
XX	ADY62117;
XX	
DT	19-MAY-2005 (first entry)
XX	
DT	Influenza A virus strain A/England/1/53 wild type NS1 gene for vaccine.
DE	
XX	
KW	protein engineering; immune stimulation; immunostimulant; vaccine;
KW	influenza virus infection; gene; ds.
XX	
OS	Influenza A virus; strain A/England/1/53.
XX	
Key	Location/Qualifiers
PH	6..719
FT	/*tag= a
CDS	/product= "influenza A virus NS1 protein"
FT	/note= "no stop codon given"
FT	
FT	

method is useful for producing a high titer reassortant influenza virus. The high titer reassortant influenza viruses are useful for producing vaccine compositions. The vaccines are useful for treating or preventing influenza viral infections. Genetic engineering techniques allow the rapid production of custom made attenuated virus vaccines, but vaccine use is limited by the need to use vaccine approved cell lines. The master strain A/PuertoRico/8/34 which is the most widely used in producing recombinant viruses for vaccine use produces a high titer in MDCK cells, which are not certified for use in production of human vaccines, but not in Vero cells, which are certified for this use. The applicants have discovered that replacing the NS gene of the A/PuertoRico/3/24 master strain with the NS gene of the A/England/1/53 strain gives reassortant virus that produces a high titer in Vero cells. This sequence corresponds to the coding sequence for the NS1 protein from the A/England/1/53 influenza strain.

SQ	Sequence	824 BP;	267 A;	167 C;	201 G;	189 T;	0 U;	0 Other;
Query Match	83.1%;	Score	573.2;	DB	14;	Length	824;	
Best Local Similarity	89.4%;	Fred.	No. 8.2e-175;					
Matches	617;	Conservative	0;	Mismatches	73;	Indels	0;	Gaps
OY	1	ATGGAATTCMAACACTGTGGTCAAGCTTTGAGTGAGACTGTTTTCTTTGGCATCTGC	CGAAA	60				
Db	6	ATGGAATCCCAACACTGTGTCAAGCTTTCAAGTAGATGCTCTCTTTGGCAATGTC	CGCAA	65				
OY	61	CGAATTGCGAGACAAGAATACTGGGTGATGCCCATTCCTTCCTGACCGGCTTC	CGCAGACCG	120				
Db	66	CNAGTTGCGAGACAAGAATACTAGGTGATGCCCATTCCTTGATCGCTCTCC	CGATCTCG	125				
OY	121	AAGTCCCCTAAAAAGGAAGGTAGACACTCTTTGGTCTGTGGACATCTGMAACAG	CGCHCTGT	180				
Db	126	AAGTCCCCTAAAGGGGAAGAGCGACACTCTCTGGTCTGMAACATCGMAAC	CGCACCCGT	185				
OY	181	GGAAAGCAGATAGTGGAGCAGATCTGGGAAGAGGAATCAGATGAGGCACTT	TAAATGACC	240				
Db	186	GGAAAGCAGATAGTGGAGAGGANTCTGAAGGAAGGAATCCGATGAGGCACT	TAAATGACC	245				
OY	241	ATTGCCCTCTGTCTCTCTCTACGCTACTTAACTGACATGACTCTTGATGAGAT	GTCAAGA	300				
Db	246	ATGGCTCTCCGACACTGCTTCGCGATACCTTAACATGACATGACTATTTGAG	GAATAATG	305				
OY	301	GACTGGTTCATGTCTCATGCCCAAGCAAAAGTAACAGGCTCCCTATCTATA	PAGAATG	360				
Db	306	GACTGGTTCATGTCTATATGCCCAAGCAAAAGTGGCAGGCCCTCTTTGTAT	"CAGAAATG	365				
OY	361	CAGGCAATCATGGATAAGAAACATCATACTTTAAAGCAAACTTTAGTGTGAT	TTTCGAAGG	420				
Db	366	CAGGCGATCATGGATAAGAAACATCATACTGAAAGCGAATTTCA GTGTGAT	TTTTTGACCG	425				
OY	421	CTGGAGACATTAATACTACTTTAGAGCCCTTCAACGAGAGGAGCAGCTGTT	GGCGAAAT	480				
Db	426	CTGGAGACCCCTAATAATTACTAAGGCGCTTTCAACGAGAGGGAGCAAT	TGTTGGCGAAAT	485				
OY	481	TCACCAATGTGCTTCTCTTCCAGGACATACTAATAGGATGTCAAAAATG	CAAAATGG	540				
Db	486	TCACCAATGTGCTTCTCTTCCAGGACATACTAATAGGATGTCAAAAATG	CAAAATGG	545				
OY	541	CTCATCGGAGACCTTAAATGGAAATGATACTACGGTTAGAAATCTCTG	AAACTCT	600				
Db	546	CTCATCGGAGACCTTGAATGGAAATGATAACACAGTTTCGAGTCTCT	TAAACTCT	605				
OY	601	TTTCGTTGGAAGACGAGTCA TGAGAAATGGGAGACCTTTCA TTCCCT	TCCAAAG	660				
Db	606	TTTCGTTGGAAGACGAGTAATGAGAAATGGGAGACCTTCCA CTCACT	CCTCCAA	665				
OY	661	AAAAATGGAGAGAACAAATTGAGCCGAGGTTT	690					
Db	666	AAAAATGGAGAGAACAAATTAGGTACGAGGTTT	695					

RESULT 8
ADO15247

CC gene, PA protein gene, NP protein gene, M protein gene and NS protein
CC gene (Axx82192-X82197). The method is useful for the production of cold-
CC adapted influenza virus that exhibit temperature sensitivity and can be
CC actively grown in fertilized eggs. The virus is useful for vaccines for
CC protection against 'flu. Live vaccines containing cold-adapted viruses
CC have several advantages over killed vaccines. It can prevent reduction of
CC immunogenicity, which may occur in the killed vaccine where antigenic
CC proteins would be denatured at its inactivation. It can also avoid
CC hypersensitivity due to the prolonged administration of heterologous
CC proteins. It promotes the immunity by inducing IGA and it can be
CC administered into a spray formulation via nasal cavity and thus its
CC application is convenient for children. It is able to inhibit the growth
CC of the wild-type virus and thus its therapeutic effect can be expected.
XX The present sequence represents the Influenza virus NS protein gene
XX
SQ Sequence 890 BP; 283 A; 179 C; 215 G; 213 T; 0 U; 0 Other;

Query Match 82.4%; Score 568.4; DB 2; Length 890;
Best Local Similarity 89.0%; Pred. No. 3.1e-173;
Matches 614; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 1 ATGGATTCCAACTGTGTCAAGCTTTTCAGGTGAGTGTCTTTTGGCATGTCGCAAA 60
DB |||||
QY 27 ATGGATCCAACTGTGTCAAGCTTTTCAGGTGAGTGTCTTTTGGCATGTCGCAAA 86
DB |||||
QY 61 CGATTTCGAGCAAGAACTGGGTGATGCCCATTTCTTGACCGCTTCGCGAGACAG 120
DB |||||
QY 87 CGAGTTGCGAGCAAGAACTAGGTGATGCCCATTTCTTGATCGGCTTCGCGAGATCAG 146
DB |||||
QY 121 AAGTCCCTAAAGGAAGAGGTAGTCACTCTTGGTCTGGACATCGAAACAGCCACTCGTGCA 180
DB |||||
QY 147 AATCCCTAAGGGAAGGGGAGTACTCTCGGTCTGGACATCAAGACAGCCACAGTGTCT 206
DB |||||
QY 181 GGAAGCAGATAGTGGAGCAGATTTCTGGAAGAGGAATCAGATGAGGCACCTTAAATGACC 240
DB |||||
QY 207 GGAAGCAGATAGTGGAGCAGATTTCTGGAAGGAAGAAATCGATGAGGCACCTTAAATGACC 266
DB |||||
QY 241 ATGGCTCTGTCTGTCTTCACTTCACTTAACTGATGATGCTCTTGATGAGATGCAAGA 300
DB |||||
QY 267 ATGGCTCTGTCTGTCTTCACTTCACTTAACTGATGATGCTCTTGATGAGATGCAAGG 326
DB |||||
QY 301 GACTGGTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTATGATATAAGATGGAC 360
DB |||||
QY 327 GACTGGTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTTGTATCAGATGGAC 386
DB |||||
QY 361 CAGGCAATCATGGATTAAGAACATCATCTTAAAGCAACTTGTAGTGTGATTTTGAAGG 420
DB |||||
QY 387 CAGGCAATCATGGATTAAGAACATCATCTTAAAGCAACTTGTAGTGTGATTTTGAAGG 446
DB |||||
QY 421 CTGGAGCACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 480
DB |||||
QY 447 CTGGAGCACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 506
DB |||||
QY 481 TCACCAATTCCTTCTTCCAGGACATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 540
DB |||||
QY 507 TCACCAATTCCTTCTTCCAGGACATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 566
DB |||||
QY 541 CTATCCGAGGACCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 600
DB |||||
QY 567 CTATCCGAGGACCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 626
DB |||||
QY 601 TTCGCTTGGAGAGCAGTCAATGAATGGAGACCTTCAATTCCTCCCTCCAAAGCAGAAACGA 660
DB |||||
QY 627 TTCGCTTGGAGAGCAGTCAATGAATGGAGACCTTCAATTCCTCCCTCCAAAGCAGAAACGA 686
DB |||||
QY 661 AAAATGGAGAGAACAAATTTGAGCCAGAGTT 690
DB |||||
QY 687 GAAATGGCGGGAACAAATTTAGTCAAGTT 716
DB |||||

RESULT 10
ADW44527
ID ADW44527 standard; cDNA; 890 BP.

XX ADW44527;
AC 24-MAR-2005 (first entry)
DT Influenza A virus NS cDNA.
XX virucide; vaccine; gene therapy; gene transfer; viral infection; NS;
XX gene; ss.
XX Influenza A virus.
OS WO2004112831-A2.
DN 29-DEC-2004.
XX 27-MAY-2004; 2004WO-US016680.
PF 28-MAY-2003; 2003US-0473798P.
XX (WISC) WISCONSIN ALUMNI RES FOUND.
XX Kawaoka Y;
XX WPI; 2005-048767/05.
DR New polynucleotide comprising a nucleic acid segment or its complement
XX encoding an influenza virus HA, NA, PB1, PB2, PA, NP, M, NS or its
XX portion, useful in preparing a vaccine composition against influenza
XX virus infection.
XX Claim 1; SEQ ID NO 6; 77pp; English.
XX The invention describes an isolated polynucleotide comprising a nucleic
XX acid segment or its complement encoding an influenza virus HA, NA, PB1,
XX PB2, PA, NP, M, NS or its portion, having substantially the same amino
XX acid sequence or activity as a corresponding polypeptide encoded by a
XX sequence comprising 233, 234, 1565, 1027, 890, 1775 or 1413 base pairs.
XX Also described are: a composition comprising influenza virus vectors;
XX preparing influenza virus; preparing a gene delivery vehicle; a cell
XX contacted with the composition or infected with the virus; a vector
XX comprising a promoter and the nucleic acid segment; immunizing an
XX individual against a pathogen; and an isolated influenza virus comprising
XX the polynucleotide. The polynucleotide is useful in preparing a vaccine
XX composition against influenza virus infection. This sequence represents
XX Influenza A virus NS cDNA.
XX
SQ Sequence 890 BP; 283 A; 181 C; 215 G; 211 T; 0 U; 0 Other;

Query Match 82.4%; Score 568.4; DB 14; Length 890;
Best Local Similarity 89.0%; Pred. No. 3.1e-173;
Matches 614; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 1 ATGGATTCCAACTGTGTCAAGCTTTTCAGGTGAGTGTCTTTTGGCATGTCGCAAA 60
DB |||||
QY 27 ATGGATCCAACTGTGTCAAGCTTTTCAGGTGAGTGTCTTTTGGCATGTCGCAAA 86
DB |||||
QY 61 CGATTTCGAGCAAGAACTGGGTGATGCCCATTTCTTGACCGCTTCGCGAGACAG 120
DB |||||
QY 87 CGAGTTGCGAGCAAGAACTAGGTGATGCCCATTTCTTGATCGGCTTCGCGAGATCAG 146
DB |||||
QY 121 AAGTCCCTAAAGGAAGAGGTAGTCACTCTTGGTCTGGACATCGAAACAGCCACTCGTGCA 180
DB |||||
QY 147 AAAATCCCTAAAGGAAGGGGAGTACTCTCGGTCTGGACATCAAGACAGCCACAGTGTCT 206
DB |||||
QY 181 GGAAGCAGATAGTGGAGCAGATTTCTGGAAGAGGAATCAGATGAGGCACCTTAAATGACC 240
DB |||||
QY 207 GGAAGCAGATAGTGGAGCAGATTTCTGGAAGGAAGAAATCGATGAGGCACCTTAAATGACC 266
DB |||||
QY 241 ATTGCTCTGTCTGTCTTCACTTCACTTAACTGATGATGCTCTTGATGAGATGCAAGA 300
DB |||||
QY 267 ATGGCTCTGTCTGTCTTCACTTCACTTAACTGATGATGCTCTTGATGAGATGCAAGG 326
DB |||||

QY 301 GACTGGTTCATGCTATGCCAGCAGAAAGTAACAGGCTCCCTATGTATATAAGAAATGGAC 360
 Db 327 GACTGGTCCATGCTCATACCCCAAGCAGAAAGTGGCAGGCCCTCTTTGTATCAGAATGGAC 386
 QY 361 CAGCAATCATGATGAAGAATCATATCTTAAAGCAAACTTTAGTGTGATTTTCGAAGG 420
 Db 387 CAGCGCATGATGAAGAATCATATCTGAAAGCGCAACTTCAGTGTGATTTTCGACCG 446
 QY 421 CTGAGAGACATTAATCTACTTTAGAGCCCTTCACCGAAGAGGAGCAGTCTGTTGCGCAAAAT 480
 Db 447 CTGAGAGACTTAATATTTGCTAAGGCTTTTCAACGAGAGGAGGACAAATTTTTCGCAAAAT 506
 QY 481 TCACCATTCCTCTCTTCCAGGACATCTAATAGAGATGTCAAAAATGCAATTTGGGGTC 540
 Db 507 TCACCATTCCTCTCTTCCAGGACATCTGCTGAGGATGTCAAAAATGCAATTTGGAGTC 566
 QY 541 CTATCGAGGACTTAATGAATGAATGAATAGCGTTTGAATCTCTGAACTCTACAGAGA 600
 Db 567 CTATCGAGGACTTGAATGAATGAATGAATAGCGTTTGAATCTCTGAACTCTACAGAGA 626
 QY 601 TTGCTTTGGAGAGCAGTCATGAGATGGGAGACCTTCATTCCTCCCAAGCAGAAAGCA 660
 Db 627 TTGCTTTGGAGAGCAGTCATGAGATGGGAGACCTTCATTCCTCCCAAGCAGAAAGCA 686
 QY 661 AAAATGGAGAGCAATTTGAGCCGAAGTT 690
 Db 687 GAAATGGCGGAGCAATTTAGGTCAGAAGTT 716

RESULT 11

AAD37061
 ID AAD37061 standard; cDNA; 890 BP.

XX AC AAD37061;

XX 21-AUG-2002 (first entry)

XX Influenza A virus/singapore/1/57/ca NS mutant cDNA.

XX Attenuated influenza vaccine; prophylactic; therapeutic; infection;
 virulence; gene; NS1 protein; NS2 protein; mutant; ss.

XX Influenza A virus.

XX Synthetic.

XX Key Location/Qualifiers

XX CDS 27..864

XX /tag= b

XX /product= "NS2 mutant protein"

XX /transl_except= (pos:48..525, aa:Asn-Leu)

XX CDS 27..740

XX /tag= a

XX /product= "NS1 mutant protein"

XX mutation replace(813, A)

XX /tag= c

XX WO200224876-A2.

XX 28-MAR-2002.

XX 25-SEP-2001; 2001WO-BF011087.

XX 25-SEP-2000; 2000EP-00120896.

XX (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.

XX Kateringer H, Egorov A, Ferko B, Romanova J, Kateringer D;

XX WPI; 2002-416282/44.

XX P-PSDB; AAE23116, AAE23117.

XX Manufacturing live vaccine, by infecting Vero cells with virus, combining
 cells with serum-free cell culture medium, incubating cells in presence

PT of protease and nuclease, harvesting virus and preparing vaccine.
 XX Example 4; Page 44; 90pp; English.
 XX The present invention relates to a method for isolating viruses from
 various sources and for producing live attenuated influenza vaccines in a
 serum-free African green monkey kidney (Vero) cell culture under
 conditions where alterations in the surface antigens of the virus due to
 adaptive selection are minimised or prevented. The method is useful for
 the manufacture of whole-virus vaccine, preferably attenuated live
 vaccine. It is useful for prophylactic or therapeutic administration
 against viral infection, preferably influenza virus infections. The
 present sequence is influenza A virus/singapore/1/57/ca (cold adapted)
 CC mutant cDNA encoding NS1 and NS2 protein. This sequence is used in the
 CC exemplification of the invention
 XX

SQ Sequence 890 BP; 294 A; 178 C; 207 G; 211 T; 0 U; 0 Other;

Query Match 82.18; Score 566.8; DB 6; Length 890;

Best Local Similarity 88.88; Pred. No. 1e-172;

Matches 613; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 1 ATGGATTCACACATGTCTCAGCTTTGAGTGTAGTCTTTCTTTGGCATGTCCGAAA 60
 Db 27 ATGGATTCCTAACACTGTCTCAGCTTTGAGTGTAGTCTTTCTTTGGCATGTCCGAAA 86
 QY 61 CGATTTCGAGACCAAGAACTGGGTGATGCCCTTCCTTCGACCGCTTCGCGAGACGAG 120
 Db 87 CAAAGTTCGAGACCAAGAACTGAGTGTATGCCCTTCCTTCGACCGCTTCGCGAGATCAG 146
 QY 121 AAGTCCCTAAAAGGAGAGGTAGTGTCTTGTCTGGACATCGAAACACCACTCTGTGCA 180
 Db 147 AAGTCCCTAAGGAGAGAGGTAGTGTCTTGTCTGGACATCGAAACACCACTCTGTGCA 206
 QY 181 CGAAAGCAGATAGTGGAGCAGATTTCTGGAAGAGAAATCAGATGAGGACCTTAAATGACC 240
 Db 207 CGAAAGCAGATAGTGGAGCAGATTTCTGGAAGAGAAATCAGATGAGGACCTTAAATGACC 266
 QY 241 ATTGCTCTGTCTCTCTTCAGCTTCTTAACTGACATGACTCTTGTGAGATGTCAAGA 300
 Db 267 ATGGCTCCGACCTCTCTTCGATACCTTAACTGACATGACTTATGAGGAAATGTCAAG 326
 QY 301 GACTGTTCATGCTCATGCCAGCAGAAAGTACAGGCTCCCTATGTATAGATGGAC 360
 Db 327 GACTGTTCATGCTTAATGCCAGCAGAAAGTGTGAGGCCCTCTTGTATCAGATGGAC 386
 QY 361 CAGCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 Db 387 CAGCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 446
 QY 421 CTGAGAGACATTAATCTACTTTAGAGCCCTTCACCGAAGAGGAGCAGTCTGTTGCGAAAT 480
 Db 447 CTAGAGACCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 506
 QY 481 TCACCATTCCTCTCTTCCAGGACATCTAATGAGGATGTCAAAAATGCAATTTGGGGTC 540
 Db 507 TCACCATTCCTCTCTTCCAGGACATCTAATGAGGATGTCAAAAATGCAATTTGGGGTC 566
 QY 541 CTATCGGAGGACTTAAATGGAATGATATACGGTGTAGAAATCTCTGAAACTCTACAGAGA 600
 Db 567 CTATCGGAGGACTTGAATGGAATGATATACGGTGTAGAAATCTCTGAAACTCTACAGAGA 626
 QY 601 TTGCTTTGGAGAGCAGTCATGAGATGGGAGACCTTCATTCCTCCCAAGCAGAAAGCA 660
 Db 627 TTGCTTTGGAGAGCAGTCATGAGATGGGAGACCTTCATTCCTCCCAAGCAGAAAGCA 686
 QY 661 AAAATGGAGAGCAATTTGAGCCGAAGTT 690
 Db 687 GAAATGGCGGAGCAATTTAGGTCAGAAGTT 716

RESULT 12
 AAO22332

ID AAQ22332 standard; DNA; 890 BP.
XX AC AAQ22332;
XX DT 14-JUL-1992 (first entry)
XX DE RNA (+), (mRNA) from influenza virus A, synthesised from segment 8.
XX KW Segments 1-8; Ann Arbor H2N2; A; B; C; transcription; ss.
XX OS Influenza A virus.
XX PN WO9203454-A.
XX PD 05-MAR-1992.
XX PF 13-AUG-1991; 91WO-US005742.
XX PR 14-AUG-1990; 90US-00567287.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Cowser LM, Ecke, Ecker DJ;
XX DR WPI; 1992-096817/12.
XX New DNA and RNA hybridising to influenza A, B or C - for diagnosis and
PT treatment of influenza, esp. influenza B.
XX PS Disclosure; Fig 5; 64pp; English.
XX The RNA sequence is derived influenza virus A, Ann Arbor strain H2N2 of
CC segment 8. The mRNA of this segment encodes the NS1 and NS2 proteins. The
CC sequence can be used to design oligonucleotide inhibitors against
CC influenza virus. See also AAQ22289-22331
XX Sequence 890 BP; 292 A; 177 C; 208 G; 0 T; 213 U; 0 Other;
SQ

Query Match 80.8%; Score 557.2; DB 2; Length 890;
Best Local Similarity 67.1%; Pred. No. 1.3e-169;
Matches 463; Conservative 144; Mismatches 83; Indels 0; Gaps 0;
1 ATGGATTCCAACTGTCTCAAGCTTTTCAGGTAGACTGTCTTTCTTTGGCATGTCGCGAAA 60
27 AUGGATCCUACACUGUGUCAAGCUUUCAGGUAGAUUGCUUUGGCAUGUGCGCAA 86
61 CGATTTGCAGACCAAGAACTGGGTGATGCCCATTCCTTGACCGGCTTCCGAGACAG 120
87 CAAGUUGCAGACCAAGAACUAGUGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 146
121 AAGTCCCTAAAGAGAGAGTAGCCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 180
147 AGUCCUAGAGGAGAGACUCACUACUUCUGUUGUAGUAGUAGUAGUAGUAGUAGUAGU 206
181 GGAAGCAGATAGTGGACAGATCTTGAAGAGAGATCAGATGAGGACCTTAAATGACC 240
207 GGAAGCAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 266
241 ATTGCTCTGTTCTGCTTACCGCTTACTTAACTGACATGACTCTTGTATGATGTCTCAGA 300
267 AUGGCTTCCGACACCGUUCGCGAUACUACUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 326
301 GACTGGTTCATGCTCATGCCCAAGCAAGAAAGTAACAGGTCCTCTATGTATATAGATGAC 360
327 GACUGGUCAUGCAUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 386
361 CAGCAATCATGATAGAAACATCATATCTTAAAGCAAACTTTAGTGTGATTTGCAAGG 420
387 CAGGCAUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 446
421 CTGAGAGACATATATCTTCTAGAGCTTCA CCGAAGAGAGAGAGAGAGAGAGAGAGAG 480
447 CUAGAGAGCCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 506

QY 481 TCACCAATGCTCTCTCTTCAGGACATACATTAATGAGGATGCTAAAAATGCAATGGGTC 540
DB 507 UCACCAATGCTCTCTCTTCAGGACATACATTAATGAGGATGCTAAAAATGCAATGGGTC 566
QY 541 CTCATCGGAGGACTTAAATGGAATGATTAACGTTAGATCTCTGAATCTTACAGAGA 600
DB 567 CUCATCGGAGGACTTAAATGGAATGATTAACGTTAGATCTCTGAATCTTACAGAGA 626
QY 601 TTCGCTTGGAGAGCAGTATGAGATGAGGAGACCTTCAATCTCCCTCCAAAGCAGAAACGA 660
DB 627 UUCGCUUGGAGAGCAGTATGAGATGAGGAGACCTTCAATCTCCCTCCAAAGCAGAAACGG 686
QY 661 AAAATGAGAGACCAATTCAGCCAGAGATT 690
DB 687 AAAAUGGCGAGAACAAUUAUGGCUCAAAAGUU 716

RESULT 13
ABA93942
ID ABA93942 standard; DNA; 890 BP.
XX AC ABA93942;
XX DT 07-MAY-2002 (first entry)
XX DE Influenza A/Udorn/72 (H3N2) Strain NS1 encoding DNA SEQ ID NO:17.
XX KW Influenza A/Udorn/72 (H3N2) strain; Influenzavirus A; diagnosis;
XX KW Influenza A virus; genome; gene; ds.
XX OS Influenzavirus A.
XX Key Location/Qualifiers
XX CDS 27..740
XX FT /*tag= a
XX FT /product= "NS1 protein"
XX WO200200884-A2.
XX PD 03-JAN-2002.
XX PF 21-JUN-2001; 2001WO-US019826.
XX PR 23-JUN-2000; 2000US-0213650P.
XX PA (AMCY) AMERICAN CYANAMID CO.
XX PI Galarza JM, Latham TE;
XX DR WPI; 2002-139923/18.
XX P-PSDB; ABB05772.
XX Polynucleotide encoding complete sequence of influenza A/Udorn/72 and
PT polypeptide, useful in diagnosis and for generating new influenza A
PT variant strains.
XX Claim 1; Page 77-78; 103pp; English.
XX The present invention describes an isolated polynucleotide (I) having the
CC complete sequence of the Influenza A/Udorn/72 (H3N2) strain in positive
CC strand, antigenomic message sense. ABA93942 to ABA93944 encode the
CC Influenza A/Udorn/72 (H3N2) strain proteins given in ABB05764 to ABB05774
CC from the present invention. (I) is useful for designing polymerase chain
CC reaction (PCR) primers for use in a PCR assay to detect the presence of
CC the corresponding virus segment in a sample or for designing and
CC selecting peptides for use in an enzyme linked immunosorbent assay to
CC detect the presence of the corresponding protein produced by that segment
CC in a sample, hence is useful in diagnosis and may be modified by mutation
CC to generate new influenza A variant strains. ABA94945 to ABA94039
CC represent Influenza A/Udorn/72 (H3N2) strain sequencing primers, which
CC are used in an example from the present invention
XX

SQ Sequence 890 BP; 296 A; 176 C; 208 G; 210 T; 0 U; 0 Other;
 Query Match 78.2%; Score 539.6; DB 6; Length 890;
 Best Local Similarity 86.4%; Pred. No. 6.8e-164;
 Matches 596; Conservative 0; Mismatches 94; Indels 0; Gaps 0;
 QY 1 ATGGATTCCAAACACTGTCTCAAGCTTTTCAGTAGACTGTTTCTTTGGCATGTCGCGAAA 60
 DB 27 ATGGATTCCAAACACTGTCTCAAGCTTTTCAGTAGACTGTTTCTTTGGCATGTCGCGAAA 86
 QY 61 CGATTTCGAGACCAAGAACTCGGTGATGCCCACTTCTTGACCGGCTTCGCGAGACAG 120
 DB 87 CAAGTTGTAGACCAAGAACTAGGTGATGCCCACTTCTTGATCGGCTTCGCGAGATCAG 146
 QY 121 AAGTCCCTAAAGGAGAGGTAGCACTCTTGCTGGATCGGATCGGAACAGGCACCTCTGCA 180
 DB 147 AAGTCTTAGGGAGAGGAGCGACCTCTCGGTCTAAATCATGAGCGCCACCAATGTT 206
 QY 181 GGAACGAGATGTGGAGCAGATTTCGGAAGAGGAAATCGATGAGGCACTTAAATGACC 240
 DB 207 GGAAGCAGATGTAGAGAGATTCTGAAGAGAGAAATCTGATGAGGCACTTAAATGACC 266
 QY 241 ATGGCTCTGTTCTCGCTTCAAGCTACTTAACTGACATGACTCTTGATGATGATGTCAGA 300
 DB 267 ATGGCTCTCACACCTGCTTCGCGATACATCACTGACATGACTTATGAGGAATGTCAGG 326
 QY 301 GACTGGTTCATCTCATGCCCAAGCAGAAAGTAACAGGCTCCCTATGTATATAAGAAATGGAC 360
 DB 327 GACTGGTTCATCTAATGCCCAAGCAGAAAGTGAAGGACCTCTTTGCATCAGAAATAGAC 386
 QY 361 CAGGCAATCATGATAAGAAATCATATCTTAAAGCAAACTTATGTGATTTTCGAAAGG 420
 DB 387 CAAGCAATCATGATAAGAAATCATATCTTGAAGCGCAATTTTCAGTGTGATTTTCAGCGG 446
 QY 421 CTGGAGACATAATACTACTTACTTAGAGCTTCCACGAGAGAGGAGCAGTCTGTGGCGAAAT 480
 DB 447 CTAGAGACCTAATATTAATTAAGGCTTTTCACCGAAGAGGAGCAATTTGTGGCGAAATC 506
 QY 481 TCACCATTCGCTTCTTCCAGGACATCTAATGAGGATGTCAAATATCAATTTGGGGTC 540
 DB 507 TCACCATTCGCTTCTTCCAGGACATCTAATGAGGATGTCAAATATCAATTTGGGGTC 566
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 QY 601 TTGCTTTGGAGAGCAGTCATGAGATGGGAGACCTTCAATTCCTCCAAAGCAGAAAGCA 660
 DB 627 TTGCTTTGGGAGAGCAGTAATGAGATGGGAGACCTTCAATTCCTCCAAAGCAGAAAGCG 686
 QY 661 AAAATGGAGAGCAAAATGAGCCAGAGATT 690
 DB 687 AAAATGGGAGAGCAGTAGTCAAAAGTT 716

RESULT 14

ID AAH77932
 XX AAH77932 standard; DNA; 906 BP.
 AC AAH77932;
 XX
 XX 13-NOV-2001 (first entry)
 XX Nucleotide sequence of PR8NS38.
 XX Nonstructural gene; NS gene; influenza A virus; NSI gene; vaccine;
 KW viral infection; influenza infection; HIV-1 infection; ss.
 XX Unidentified.
 XX
 XX WO200164860-A2.
 XX
 PD 07-SEP-2001.

XX 02-MAR-2001, 2001WO-EP002392.
 PF 02-MAR-2000, 2000EP-00104338.
 PR (POLY-) POLYMER SCI IMMUNOBIOLOGISCHE FORSCHUNG.
 PA Ferko B, Egorov A, Voglauer R;
 PI WPI; 2001-514840/56.
 XX
 XX Recombinant NS gene of an influenza A virus comprising a functional RNA
 binding domain and a gene sequence modification after nucleotide position
 100 of the NSI gene segment, useful for producing a live attenuated
 influenza virus vaccine.
 PT
 PT
 PT
 XX Example 6; Page 21; 40pp; English.
 XX The specification describes a recombinant nonstructural (NS) gene of an
 influenza A virus. The gene comprises a functional RNA binding domain and
 a gene sequence modification after nucleotide position 400 of the NSI
 gene segment, counted on the basis of influenza A/PR/8/34 virus, where
 the modification bars transcription of the remaining portion of the NSI
 gene segment. The recombinant NS gene is used to produce a vaccine, which
 is useful for prophylactic or therapeutic application against a viral
 infection, preferably against influenza or HIV-1 infection. Influenza
 virus transfectants that contain the modified NS gene may have an
 interferon (IFN) inducing phenotype, but may or may not be sensitive
 towards IFN. The present sequence was used to construct vectors for
 production of modified NS genes of the invention
 CC
 SQ Sequence 906 BP; 288 A; 183 C; 221 G; 214 T; 0 U; 0 Other;

Query Match 77.2%; Score 532.4; DB 4; Length 906;
 Best Local Similarity 87.0%; Pred. No. 1.5e-161;
 Matches 614; Conservative 0; Mismatches 76; Indels 16; Gaps 2;
 QY 1 ATGGATTCCAAACACTGTCTCAAGCTTTTCAGTAGACTGTTTCTTTGGCATGTCGCGAAA 60
 DB 27 ATGGATTCCAAACACTGTCTCAAGCTTTTCAGTAGACTGTTTCTTTGGCATGTCGCGAAA 86
 QY 61 CGATTTCGAGACCAAGAACTCGGTGATGCCCACTTCTTGACCGGCTTCGCGAGACAG 115
 DB 87 CAGTTTCGAGACCAAGAACTAGGTGATGCCCACTTCTTGATCGGCTTCGCGAGTGAAT 146
 QY 116 -----ACGAGAGTCCCTTAAAGAGAGAGTAGCACTTTGGTCTGGACATCGAA 165
 DB 147 AACTAGCTGAATCAGAAATCCCTAGAGAGAGGGGCGAGCACCTCTCGTCTGGACATCGAG 206
 QY 166 ACAGCCACTCTGCGAGAAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATCAG 225
 DB 207 ACAGCCACACGCTGCTGGAAGAGCAGATAGTGGAGCGGATCTTGAAGAGAAATCCGATGAG 266
 QY 226 GCACCTTAAATGACCATGCTCTGTTCTCTCTCAAGCTTAACTGACATGACTCTT 285
 DB 267 GCACCTTAAATGACCATGCTCTGTTCTCTCTCAAGCTTAACTGACATGACTCTT 326
 QY 286 GATGAGATGTCAAGAGACTGTTTCTGATGCTGCTTCCAGCAGAGAAATGTAACAGGCTCCCTA 345
 DB 327 GAGGAAATGTCAAGGACTGGTCCATGCTCATCCCAAGCAGAAAGTGGCAGGCTCTT 386
 QY 346 TGTATAAGAAATGGACAGGCAATCATGGA-TAAGAAATCATCTACTTAAAGCAAACTTTAG 404
 DB 387 TGTATCAGAAATGGACAGGCAATCATGGA-TAAGAAATCATCTACTTAAAGCAAACTTTAG 446
 QY 405 TGTGATTTTCCAAAGGCTGGAGACACTTAATCTACTTACTTAGAGCTTCAACCGRAGAGGAC 464
 DB 447 TGTGATTTTCCAAAGGCTGGAGACACTTAATCTACTTACTTAGAGCTTCAACCGRAGAGGAC 506
 QY 465 AGTCGTTGGCGAAATTTCCACCATGCTCTCTTCTTCCAGGACATCTAATGAGAGATGTCAA 524
 DB 507 AATTGTTGGCGAAATTTCCACCATGCTCTCTTCTTCCAGGACATCTAATGAGAGATGTCAA 566

Qy	525	AAATGCAATCGGGTCTCATCGGAGGACTTAAATGGAATGATAATACGGTTAGATCTC	581
Db	567	AAATGCAATCGGGTCTCATCGGAGGACTTAAATGGAATGATAATACGGTTAGATCTC	626
Qy	585	TGAACTCTCAGAGAGATTCGCTTGGAGAGCAGTCAATGAGAATGGAGACCTTCATTCC	644
Db	627	TGAACTCTCAGAGAGATTCGCTTGGAGAGCAGTCAATGAGAATGGAGACCTTCACATC	686
Qy	645	TCCAAAGCAGAAACGAAAAATGGAGAGACAAATTGAGCCGAAAGTT	690
Db	687	TCAAAAACAGAAACGAGAAATGCGCGGGAACAATTAGGTCAGAAAGTT	732
RESULT 15			
AAAD15680	ID	AAAD15680 standard; DNA; 468 BP.	
XX	AC	AAAD15680;	
XX	DT	15-NOV-2001 (first entry)	
XX	DE	Equine influenza virus H3N8 neiwt4NS468 DNA.	
XX	KW	Equine influenza virus; ei; cold adaptation; temperature sensitivity;	
XX	KW	vaccine; neiwt4NS468 DNA; Peiwt4NS97 protein; ds.	
XX	OS	Equine influenza virus H3N8.	
XX	Key	Location/Qualifiers	
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FT		/note= "This region is specifically claimed as SEQ ID NO: 38 in claim 2 of the specification"	
FT	CDS	3..296	
FT		/*tag= a	
FT		/product= "Peiwt4NS97 protein /note "CDS does not include start codon"	
FT		/partial	
XX	XX		
XX	PN	WO200160849-A2.	
XX	PD	23-AUG-2001.	
XX	PP	16-FEB-2001; 2001WO-US005048.	
XX	PP	16-FEB-2000; 2000US-00506286.	
XX	PA	(UIPI-) UNIV PITTSBURGH.	
XX	PI	Dowling PW, Youngner JS;	
XX	WPI	2001-522584/57.	
XX	P-PSDB	AAE09028.	
XX	XX		
XX	XX	Novel isolated equine influenza virus (wild-type and cold-adapted) proteins and viruses containing nucleic acid molecules encoding the proteins, which are useful for protecting animals from influenza virus infections.	
XX	Claim 2	Page 74-75; 172pp; English.	
XX	XX	The patent discloses cold-adapted equine influenza viruses and reasortant influenza A viruses comprising at least one genome segment of such an equine influenza virus, wherein the equine influenza virus genome segment confers at least one identifying phenotype of the cold-adapted equine influenza virus, such as cold adaptation, temperature sensitivity, dominant interference or attenuation. The viruses are useful for protecting animals from diseases caused by influenza viruses. They are also used as vaccines. The present sequence is equine influenza (ei) virus H3N8 neiwt4 (wild type) NS468 DNA encoding Peiwt4NS97 protein	
XX	Sequence	468 BP; 168 A; 80 C; 98 G; 122 T; 0 U; 0 Other;	

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QM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 00:04:28 ; Search time 3553.19 Seconds
(without alignments)
11038.514 Million cell updates/sec

Title: US-10-734-373-59

Perfect score: 690

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: gb_ba.*

2: gb_in.*

3: gb_env.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pr.*

9: gb_ro.*

10: gb_sta.*

11: gb_sy.*

12: gb_un.*

13: gb_vl.*

14: gb_hg.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	690	100.0	690	6	AR254670	AR254670 Sequence
3	690	100.0	690	6	AR455540	AR455540 Sequence
4	690	100.0	690	6	AR455545	AR455545 Sequence
5	690	100.0	690	6	AR225024	AR225024 Sequence
6	690	100.0	690	6	AR225031	AR225031 Sequence
7	690	100.0	888	6	AR254666	AR254666 Sequence
8	690	100.0	888	6	AR254669	AR254669 Sequence
9	690	100.0	888	6	AR455541	AR455541 Sequence
10	690	100.0	888	6	AR455544	AR455544 Sequence
11	690	100.0	888	6	AR225025	AR225025 Sequence
12	690	100.0	888	6	AR225029	AR225029 Sequence
13	690	100.0	891	6	AR254664	AR254664 Sequence
14	690	100.0	891	6	AR455539	AR455539 Sequence
15	690	100.0	891	6	AR225022	AR225022 Sequence
16	686.4	99.8	838	13	AF001666	AF001666 Influenza
17	688.4	99.8	838	13	AF001668	AF001668 Influenza
18	686.8	99.5	838	13	AF001667	AF001667 Influenza

19	686.8	99.5	838	13	AF001671	AF001671 Influenza
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23	682	98.8	693	13	EIVNS1	X80060 Influenza A
24	682	98.8	890	13	FLANSEROUTE	M80973 Influenza A
25	680.4	98.6	838	13	AF001664	AF001664 Influenza
26	677.2	98.1	838	13	AF001662	AF001662 Influenza
27	677.2	98.1	838	13	AF001670	AF001670 Influenza
28	674	97.7	808	13	IAU49487	U49487 Influenza A
29	674	97.7	890	13	FLANSEOKEN	M80971 Influenza A
30	672.4	97.4	890	13	FLANSEOLON	M80954 Influenza A
31	672.4	97.4	890	13	FLANSEOUNM	M80955 Influenza A
32	670.8	97.2	890	13	FLANSEONY	M80975 Influenza A
33	667.6	96.8	693	13	EIN430785	AJ430785 Influenza
34	667.6	96.8	890	13	AY328471	AY328471 Influenza
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36	667.6	96.8	890	13	FLANSEQCOR	M80953 Influenza A
37	667.6	96.8	890	13	FLANSEQSAN	M80972 Influenza A
38	666	96.5	838	13	AF001663	AF001663 Influenza
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42	661.2	95.8	890	13	IAU85376	U85376 Influenza A
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ALIGNMENTS

RESULT 1
AR254665 AR254665 690 bp DNA linear PAT 20-DEC-2002
LOCUS Sequence 52 from patent US 6482414.
DEFINITION
ACCESSION AR254665
VERSION AR254665.1 GI:27303686
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS Dowling,P.W. and Youngner,J.S.
TITLE Cold-adapted equine influenza viruses
JOURNAL Patent: US 6482414-A 52 19-NOV-2002;
The University of Pittsburgh-of the Commonwealth System of Higher Education, Pittsburgh, PA

FEATURES
source 1..690
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match	100.0%;	Score 690;	DB 6;	Length 690;
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Gaps	0;			
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Db	1	ATGGATTCCAACACTGTGTCAAGCTTTCAGGTAGACTGTTTCTTTGGCATCTCGCAAA	60	
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Db	61	CGATTTCAGACCAAGAACTGGGTGATGCCATTCCTTCACCGGCTTCGCCGAGACCAG	120	
Qy	121	AGTCCCTTAAAGAGAGGAGTACCTCTTGGTCTGACATCGAACACGACCTCGTGCA	180	
Db	121	AGTCCCTTAAAGAGAGGAGTACCTCTTGGTCTGACATCGAACACGACCTCGTGCA	180	
Qy	181	GGAAGCAGATAGTGGAGCAGATTCTTGGAGAGGAGTACATGAGGCACCTTAATGACC	240	
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QY 661 AAAATGGAGAGAACAAATGAGCCAGAGTT 690
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RESULT 2
AR254670 LOCUS
DEFINITION Sequence 59 from patent US 6482414.
ACCESSION AR254670
VERSION AR254670.1 GI:27303691

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 690)
AUTHORS Dowling, P.W. and Youngner, J.S.
TITLE Cold-adapted equine influenza viruses
JOURNAL Patent: US 6482414-A 59 19-NOV-2002;
The University of Pittsburgh-of the Commonwealth System of Higher Education; Pittsburgh, PA
FEATURES
source
1 .690
/organism="unknown"
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ORIGIN

Query Match 100.0%; Score 690; DB 6; Length 690;
Best Local Similarity 100.0%; Pred. No. 4.3e-191;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGAATCCAACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTGGCATGTCCGAAA 60
Db 1 ATGGAATCCAACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTGGCATGTCCGAAA 60
QY 61 CGATTTTCAGACCAAGAACTGGGTGATGCCCATTCCTTGACCGGCTTCGCGAGACGAG 120
Db 61 CGATTTTCAGACCAAGAACTGGGTGATGCCCATTCCTTGACCGGCTTCGCGAGACGAG 120
QY 121 AAGTCCCTTAAAGGAAGAGGTAGCACTCTTGGTCTCGACATCGAAACAGGCACTCGTGA 180
Db 121 AAGTCCCTTAAAGGAAGAGGTAGCACTCTTGGTCTCGACATCGAAACAGGCACTCGTGA 180
QY 181 GGAAGACAGATAGTGGAGCAGATTCTCGAAGAGGAATCAGATGAGGACACTTAAATGACC 240
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Db 181 GGAAGACAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGGACCTTAAATGACC 240
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Db 241 ATTGCTCTGTTCTGCTTCAAGTACTTAACTGACATGACTCTTGATGAGATGTCAAGA 300
QY 301 GACTGTTTCATGCTCATGCCCAAGCAGAAAGTAACAGGCTCCCTATGTATGAAGATGGAC 360
Db 301 GACTGTTTCATGCTCATGCCCAAGCAGAAAGTAACAGGCTCCCTATGTATGAAGATGGAC 360
QY 361 CAGGCAATCATGGATAGAACATCACTTAAAGCAAACTTTAGTGTGATTTTCGAAAGG 420
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QY 421 CTGGAGACACTTAATCTTCTAGAGGCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
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QY 541 CTATCGGAGGACTTAATGGAATGATATACGGTTAGAACTCTGAACTCTACAGAGA 600
Db 541 CTATCGGAGGACTTAATGGAATGATATACGGTTAGAACTCTGAACTCTACAGAGA 600
QY 601 TTCGCTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Db 601 TTCGCTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
QY 661 AAAATGGAGAGAACAAATGAGCCAGAGTT 690
Db 661 AAAATGGAGAGAACAAATGAGCCAGAGTT 690
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RESULT 3
AR455540 LOCUS
DEFINITION Sequence 52 from patent US 6685946.
ACCESSION AR455540
VERSION AR455540.1 GI:42690360

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 690)
AUTHORS Dowling, P.W. and Youngner, J.S.
TITLE Cold-adapted equine influenza viruses
JOURNAL Patent: US 6685946-A 52 03-FEB-2004;
The University of Pittsburgh-of the Commonwealth System of Higher Education; Pittsburgh, PA
FEATURES
source
1 .690
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 690; DB 6; Length 690;
Best Local Similarity 100.0%; Pred. No. 4.3e-191;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGAATCCAACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTGGCATGTCCGAAA 60
Db 1 ATGGAATCCAACTGTGTCAAGCTTTTCAGGTAGACTGTTTCTTGGCATGTCCGAAA 60
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QY 121 AAGTCCCTTAAAGGAAGAGGTAGCACTCTTGGTCTCGACATCGAAACAGGCACTCGTGA 180
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QY 181 GAAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGGACCTTAAATGACC 240
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 QY 241 ATTGCTCTGTTCTGCTTCACTTAATGATGAGTGTCAAGA 300
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 QY 301 GACTGGTTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTATGTATAAGATGGAC 360
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 DB 361 CAGGCAATCATGATTAAGAACATCATACTTAAAGCAAACTTTAGTGTGATTTTGGAAAGG 420
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 DB 421 CTGGAGACACTTAATGATGAGGCTTCAAGGAGGAGGAGGAGTGTGGGGAATT 480
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 DB 481 TCACGATGCTTCTTCCAGGACACTTAAAGGAGTGTCAAAATGCAATTTGGGTC 540
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 DB 601 TTGCTTGGAGAGCAGTCAATGAGAAATGGAGACCTTCATTCCCTCCAAAGCAGAAACGA 660
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 DB 661 AAAATGGAGAGCAAAATTTGAGCCAGAGTT 690

RESULT 4

AR455545
 LOCUS AR455545 690 bp DNA linear PAT 20-FEB-2004
 DEFINITION Sequence 59 from patent US 6685946.
 ACCESSION AR455545
 VERSION AR455545.1 GI:42690365
 KEYWORDS Unknown.
 SOURCE Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 690)

Dowling,P.W. and Youngner,J.S.

Cold-adapted equine influenza viruses

Patent: US 6685946-A 59 03-FEB-2004;

The University of Pittsburgh-of the Commonwealth System of Higher

Education; Pittsburgh, PA

FEATURES

source

1. .690

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 690; DB 6; Length 690;
 Best Local Similarity 100.0%; Pred. No. 4.3e-191;
 Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGATTTCCACACCTGTCTCAGCTTTCAGTGTAGTCTGTTCTTGGCATGTCGCGAAA 60
 DB 1 ATGATTTCCACACCTGTCTCAGCTTTCAGTGTAGTCTGTTCTTGGCATGTCGCGAAA 60
 QY 61 CGATTTTCAGACCCAGAACTGGGTGTAGTCCCATCTTGTAGCGGGTCTCGCGAGACGAG 120
 DB 61 CGATTTTCAGACCCAGAACTGGGTGTAGTCCCATCTTGTAGCGGGTCTCGCGAGACGAG 120
 QY 121 AAGTCCCTAAAGGAGAGGAGTGTAGTCTTGTGTGACATCGAAGAACAGCCACTGTGTGA 180

DB 121 AAGTCCCTAAAGGAGAGGAGTGTAGTCTTGTGTGACATCGAAGAACAGCCACTGTGTGA 180
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 DB 181 GAAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGGACCTTAAATGACC 240
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 QY 301 GACTGGTTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTATGTATAAGATGGAC 360
 DB 301 GACTGGTTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTATGTATAAGATGGAC 360
 QY 361 CAGGCAATCATGATTAAGAACATCATACTTAAAGCAAACTTTAGTGTGATTTTGGAAAGG 420
 DB 361 CAGGCAATCATGATTAAGAACATCATACTTAAAGCAAACTTTAGTGTGATTTTGGAAAGG 420
 QY 421 CTGGAGACACTTAATGATGAGGCTTCAAGGAGGAGGAGGAGTGTGGGGAATT 480
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 QY 661 AAAATGGAGAGCAAAATTTGAGCCAGAGTT 690
 DB 661 AAAATGGAGAGCAAAATTTGAGCCAGAGTT 690

RESULT 5

AX225024
 LOCUS AX225024 690 bp DNA linear PAT 10-SEP-2001
 DEFINITION Sequence 34 from Patent WO0160849.
 ACCESSION AX225024
 VERSION AX225024.1 GI:15555097
 KEYWORDS Equine influenza virus H3N8
 SOURCE Equine influenza virus H3N8
 ORGANISM Viruses; sRNA negative-strand viruses; Orthomyxoviridae;
 Influenzavirus A.

REFERENCE

1

Dowling,P.W. and Youngner,J.S.

Cold-adapted equine influenza viruses

Patent: WO 0160849-A 34 23-AUG-2001;

UNIV. OF PITTSBURGH OF THE COMMONWEALTH SYSTEM OF HIGHER EDUCATION

(US)

FEATURES

source

1. .690

/organism="Equine influenza virus H3N8"

/mol_type="unassigned DNA"

/db_xref="taxon:31660"

ORIGIN

Query Match 100.0%; Score 690; DB 6; Length 690;
 Best Local Similarity 100.0%; Pred. No. 4.3e-191;
 Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGATTTCCACACCTGTCTCAGCTTTCAGTGTAGTCTGTTCTTGGCATGTCGCGAAA 60
 DB 1 ATGATTTCCACACCTGTCTCAGCTTTCAGTGTAGTCTGTTCTTGGCATGTCGCGAAA 60
 QY 61 CGATTTTCAGACCCAGAACTGGGTGTAGTCCCATCTTGTAGCGGGTCTCGCGAGACGAG 120
 DB 61 CGATTTTCAGACCCAGAACTGGGTGTAGTCCCATCTTGTAGCGGGTCTCGCGAGACGAG 120
 QY 121 AAGTCCCTAAAGGAGAGGAGTGTAGTCTTGTGTGACATCGAAGAACAGCCACTGTGTGA 180

QY	1	ATGGAATTC	CAACACTG	GTCAAGCTTT	CAGGTAGAC	TGTTTCTTT	TGGCATGT	CCGCAGAA	60
Db	25	ATGGAATTC	CAACACTG	GTCAAGCTTT	CAGGTAGAC	TGTTTCTTT	TGGCATGT	CCGCAGAA	84
QY	61	CGATTTG	CAGACCA	AGAAGTCT	GGTGTAG	TGCCCATCT	TTGACCGGT	CTCCGCGAGACG	120
Db	85	CGATTTG	CAGACCA	AGAAGTCT	GGTGTAG	TGCCCATCT	TTGACCGGT	CTCCGCGAGACG	144
QY	121	AAGTCCCT	TAAGAAG	AGAGGTAG	CACACTCT	TGTGTCTG	GCATCGGAAC	ACGCACTCGTGCA	180
Db	145	AAGTCCCT	TAAGAAG	AGAGGTAG	CACACTCT	TGTGTCTG	GCATCGGAAC	ACGCACTCGTGCA	204
QY	181	GGAAAGC	AGATAG	TGGAGCAG	AATCTGGAAG	AGGAATC	CAGATGAGGC	CACTTAAATGACC	240
Db	205	GGAAAGC	AGATAG	TGGAGCAG	AATCTGGAAG	AGGAATC	CAGATGAGGC	CACTTAAATGACC	264
QY	241	ATTGCGT	CTCTGT	TCTGTCT	TCAGCTACT	TAACTGAC	TGACATGCT	TTGATCAGAGTGTCAAGA	300
Db	265	ATTGCGT	CTCTGT	TCTGTCT	TCAGCTACT	TAACTGAC	TGACATGCT	TTGATCAGAGTGTCAAGA	324
QY	301	GACTGGT	TTCATG	CTCAGC	CAAGCAG	AAAGTAA	CAGCGTCC	CTCTATGATTAAGAATGGAC	360
Db	325	GACTGGT	TTCATG	CTCAGC	CAAGCAG	AAAGTAA	CAGCGTCC	CTCTATGATTAAGAATGGAC	384
QY	361	CAGGCNA	T	CATGGAT	TAAGAA	CATCAT	ACTTAAAG	CAAACTTTAGTGTGATTTTCGAAGA	420
Db	385	CAGGCNA	T	CATGGAT	TAAGAA	CATCAT	ACTTAAAG	CAAACTTTAGTGTGATTTTCGAAGA	444
QY	421	CTGGAGAC	TAATACT	ACTTAGAG	CCTTAC	CCGAGAG	AGGACG	ACGTCTGCTGGCGCAATTT	480
Db	445	CTGGAGAC	TAATACT	ACTTAGAG	CCTTAC	CCGAGAG	AGGACG	ACGTCTGCTGGCGCAATTT	504
QY	481	TCACCA	TTGCC	TCTCTT	CCAGC	ACATACT	TAATGAG	ATGTCAAAATCGAATTTGGGGTC	540
Db	505	TCACCA	TTGCC	TCTCTT	CCAGC	ACATACT	TAATGAG	ATGTCAAAATCGAATTTGGGGTC	564
QY	541	CTCAT	CGAGGAC	CTAAA	TGGAAT	GATTAAT	ACGGTTAG	AACTCTCTGCAAACTCTACAGAG	600
Db	565	CTCAT	CGAGGAC	CTAAA	TGGAAT	GATTAAT	ACGGTTAG	AACTCTCTGCAAACTCTACAGAG	624
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Db	625	TTTCGCT	TGGAGAC	GATG	CA	TGAGAA	TGGGAG	ACCTTCATTTCCCTCCAAAGCAGAAACGA	684
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Db	685	AAAA	TGGAG	AA	CAAT	TGAG	CC	GAAGTT	714

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RESULT 8
AR254669
LOCUS
DEFINITION Sequence 57 from patent US 6482414.
ACCESSION AR254669
VERSION AR254669.1 GI:27303690
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 888)
AUTHORS Dowling,P.W. and Youngner,J.S.
TITLE Cold-adapted equine influenza viruses
JOURNAL Patent: US 6482414-A 57 19-NOV-2002;
The University of Pittsburgh-of the Commonwealth System of Higher
Education; Pittsburgh, PA
FEATURES
source
1..888
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 690; DB 6; Length 888;

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Best Local Similarity	100.0%; Pred. No. 4.3e-191;	Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1	ATGGATTCCAAACACTGTGTCAAGCTTTCAGGTAGACTGTCTTTCTTTGGCAGTGTCCGAAA 60
Db	27	ATGGATTCCAAACACTGTGTCAAGCTTTCAGGTAGACTGTCTTTCTTTGGCAGTGTCCGAAA 86
QY	61	CGATTTCGACACCAAGAACTCGGGTGATGCCCATTCCTTTGACCGGCTTCGTCGAGACGAG 120
Db	87	CGATTTCGACACCAAGAACTCGGGTGATGCCCATTCCTTTGACCGGCTTCGTCGAGACGAG 146
QY	121	AAGTCCTTAAAGGAAAGGAGGTAGACACTCTTGTGCTTGGACATCGAAACACGCCACTCGTGCA 180
Db	147	AAGTCCTTAAAGGAAAGGAGGTAGACACTCTTGTGCTTGGACATCGAAACACGCCACTCGTGCA 206
QY	181	GGAAAGCAGATAGTCGACGAGATTCTTGGAAAGAGGAATCAGATGAGCGCACTTAAATGATGCC 240
Db	207	GGAAAGCAGATAGTCGACGAGATTCTTGGAAAGAGGAATCAGATGAGCGCACTTAAATGATGCC 266
QY	241	ATTGCGCTCTGTTCTCTGCTTCAACGCTACTTAACTGACATGACTCTTGTATGAGATGTCAAAGA 300
Db	267	ATTGCGCTCTGTTCTCTGCTTCAACGCTACTTAACTGACATGACTCTTGTATGAGATGTCAAAGA 326
QY	301	GACTGGTTCATGCTCATGSCCCCAAGCAAGAAAGTAAACAGGCTCCCTATGTATATAAGAAATGGAC 360
Db	327	GACTGGTTCATGCTCATGSCCCCAAGCAAGAAAGTAAACAGGCTCCCTATGTATATAAGAAATGGAC 386
QY	361	CAGGCAATCATCGATAGACACACNTCATCTTAAAGCAAACTTTAGTGTGATTTTCGAAAGG 420
Db	387	CAGGCAATCATCGATAGACACACNTCATCTTAAAGCAAACTTTAGTGTGATTTTCGAAAGG 446
QY	421	CTGAGACACATACTACTTACTTATAGAGCTTACCGAAGAGGACGACGTCTGTTCGCGAAATT 480
Db	447	CTGAGACACATACTACTTACTTATAGAGCTTACCGAAGAGGACGACGTCTGTTCGCGAAATT 506
QY	481	TCACCAATGCCCTTCTCTTCCAGGACATATCATATGAGGATGTCAAAATATGCAATTCGGGTGC 540
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QY	541	CTCATCGGAGGACTTAAATGGAATGATTAATACGGTTAGAAATCTCTGAAAATCTTACAGAGA 600
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Db	627	TTGCGCTTGGAGAAGCAGTCATGAGAATGGGAGACCTTCAATTCCTCCAAAGCAGAGAAACGA 686
QY	661	AAATGAGAGAGAACAAATTTGAGCCACAGAAGTT 690
Db	687	AAATGAGAGAGAACAAATTTGAGCCACAGAAGTT 716

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RESULT 9
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DEFINITION Sequence 53 from patent US 6685946.
ACCESSION AR455541
VERSION AR455541.1 GI:42690361
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 888)
AUTHORS Dowling,P.W. and Youngner,J.S.
TITLE Cold-adapted equine influenza viruses
JOURNAL Patent: US 6685946-A 53 03-FEB-2004;
The University of Pittsburgh-of the Commonwealth System of Higher
Education; Pittsburgh, PA
FEATURES
source Location/Qualifiers
1..888
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/mol_type="genomic DNA"
ORIGIN

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QY	1	ATGGATTCCAACTGTCGACAGCTTCAGGTAGACGTTCTTTGGCATGTCGCGAAA	60
DB	25	ATGGATTCCAACTGTCGACAGCTTCAGGTAGACGTTCTTTGGCATGTCGCGAAA	84
QY	61	CGATTTCGAGACCAAGAACTGGGTGATGCGCCATTCCTGACCGGCTTCGCGAGACG	120
DB	85	CGATTTCGAGACCAAGAACTGGGTGATGCGCCATTCCTGACCGGCTTCGCGAGACG	144
QY	121	AAGTCCCTAAAAGGAAGAGGTAGCACTCTTGCTGTGACATCGAAGACGACCTCGTGA	180
DB	145	AAGTCCCTAAAAGGAAGAGGTAGCACTCTTGCTGTGACATCGAAGACGACCTCGTGA	204
QY	181	GGAAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGGCACTTAAATGACC	240
DB	205	GGAAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGGCACTTAAATGACC	264
QY	241	ATTGCTCTGTTCTGCTTCAAGCTTAACTGACATGACTCTTGATGAGATGTCAAGA	300
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QY	361	CAGCAATCATGATAAGAACATCATACTTAAAGCAAACTTTAGTGTGATTTTGGAAAGG	420
DB	385	CAGCAATCATGATAAGAACATCATACTTAAAGCAAACTTTAGTGTGATTTTGGAAAGG	444
QY	421	CTGAGACACTAATACTACTTACGCTTCAAGCAATGAGGAGGAGGAGTCTGTTGGCGAAAT	480
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QY	481	TCACATTGCTTCTCTCCAGGACATCTAATGAGGAGTGTCAAAATGCAATTTGGGGTC	540
DB	505	TCACATTGCTTCTCTCCAGGACATCTAATGAGGAGTGTCAAAATGCAATTTGGGGTC	564
QY	541	CTCATCGGAGACTTAAATGGAATGATAATACGTTTGAATCTCTGAAATCTTACAGAGA	600
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QY	601	TTGCTTTGGAGAGCAGTCATGAGATGGGAGACCTTCATTCCCTCCAAAGCAGAAACGA	660
DB	625	TTGCTTTGGAGAGCAGTCATGAGATGGGAGACCTTCATTCCCTCCAAAGCAGAAACGA	684
QY	661	AAATGGAGAGACAAATTCAGCCAGAGTT	690
DB	685	AAATGGAGAGACAAATTCAGCCAGAGTT	714

RESULT 10
AR45544
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

AR45544
Sequence 57 from patent US 6685946.
AR45544.1 GI:42690364
Unknown.
Unclassified.
1 (bases 1 to 888)
Dowling, P.W. and Youngner, J.S.
Cold-adapted equine influenza viruses
Patent: US 6685946-A 57 03-FEB-2004;
The University of Pittsburgh-of the Commonwealth System of Higher
Education; Pittsburgh, PA
Location/Qualifiers
1..888
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		Best Local Similarity 100.0%; Score 690; DB 6; Length 888;	
		Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	ATGGATTCCAACTGTCGACAGCTTCAGGTAGACGTTCTTTGGCATGTCGCGAAA	60
DB	25	ATGGATTCCAACTGTCGACAGCTTCAGGTAGACGTTCTTTGGCATGTCGCGAAA	84
QY	61	CGATTTCGAGACCAAGAACTGGGTGATGCGCCATTCCTGACCGGCTTCGCGAGACG	120
DB	85	CGATTTCGAGACCAAGAACTGGGTGATGCGCCATTCCTGACCGGCTTCGCGAGACG	144
QY	121	AAGTCCCTAAAAGGAAGAGGTAGCACTCTTGCTGTGACATCGAAGACGACCTCGTGA	180
DB	145	AAGTCCCTAAAAGGAAGAGGTAGCACTCTTGCTGTGACATCGAAGACGACCTCGTGA	204
QY	181	GGAAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGGCACTTAAATGACC	240
DB	205	GGAAAGCAGATAGTGGAGCAGATTCTGGAAGAGGAATCAGATGAGGCACTTAAATGACC	264
QY	241	ATTGCTCTGTTCTGCTTCAAGCTTAACTGACATGACTCTTGATGAGATGTCAAGA	300
DB	265	ATTGCTCTGTTCTGCTTCAAGCTTAACTGACATGACTCTTGATGAGATGTCAAGA	324
QY	301	GACTGGTTCATGCTCATGCCCAAGCAGAAAGTAAACAGGCTCCCTATGTATAAGATGGAC	360
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QY	361	CAGCAATCATGATAAGAACATCATACTTAAAGCAAACTTTAGTGTGATTTTGGAAAGG	420
DB	385	CAGCAATCATGATAAGAACATCATACTTAAAGCAAACTTTAGTGTGATTTTGGAAAGG	444
QY	421	CTGAGACACTAATACTACTTACGCTTCAAGCAATGAGGAGGAGGAGTCTGTTGGCGAAAT	480
DB	445	CTGAGACACTAATACTACTTACGCTTCAAGCAATGAGGAGGAGGAGTCTGTTGGCGAAAT	504
QY	481	TCACATTGCTTCTCTCCAGGACATCTAATGAGGAGTGTCAAAATGCAATTTGGGGTC	540
DB	505	TCACATTGCTTCTCTCCAGGACATCTAATGAGGAGTGTCAAAATGCAATTTGGGGTC	564
QY	541	CTCATCGGAGACTTAAATGGAATGATAATACGTTTGAATCTCTGAAATCTTACAGAGA	600
DB	565	CTCATCGGAGACTTAAATGGAATGATAATACGTTTGAATCTCTGAAATCTTACAGAGA	624
QY	601	TTGCTTTGGAGAGCAGTCATGAGATGGGAGACCTTCATTCCCTCCAAAGCAGAAACGA	660
DB	625	TTGCTTTGGAGAGCAGTCATGAGATGGGAGACCTTCATTCCCTCCAAAGCAGAAACGA	684
QY	661	AAATGGAGAGACAAATTCAGCCAGAGTT	690
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RESULT 11
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

AX225025
Sequence 35 from Patent WO0160849.
AX225025
AX225025.1 GI:15555098
Equine influenza virus H3N8
Equine influenza virus H3N8
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A.
1
Dowling, P.W. and Youngner, J.S.
Cold-adapted equine influenza viruses
Patent: WO 0160849-A 35 23-AUG-2001;
UNIV. OF PITTSBURGH OF THE COMMONWEALTH SYSTEM OF HIGHER EDUCATION
(US)

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Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 690; DB 6; Length 888;
Best Local Similarity 100.0%; Pred. No. 4.3e-191;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGATTCACACACTGTGTCAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCGCAAA 60
DB 25 ATGGATTCACACACTGTGTCAGCTTTTCAGGTAGACTGTTTCTTTGGCATGTCGCAAA 84
QY 61 CGATTTGACAGCACTGAGTGGTATGCCCATCTTTCAGCGGCTTCGCGAGACGAG 120
DB 85 CGATTTGACAGCACTGAGTGGTATGCCCATCTTTCAGCGGCTTCGCGAGACGAG 144
QY 121 AAGTCCCTAAAGAGAGAGTGAAGTCTTGGTGTGAGCATCGAAAGAGGACCTGTGCA 180
DB 145 AAGTCCCTAAAGAGAGAGTGAAGTCTTGGTGTGAGCATCGAAAGAGGACCTGTGCA 204
QY 181 GGAAGAGAGATGAGGAGAGATCTGGAAGAGAGATTCAGATGAGGCACTTAAATGACC 240
DB 205 GGAAGAGAGATGAGGAGAGATCTGGAAGAGAGATTCAGATGAGGCACTTAAATGACC 264
QY 241 ATTGCTCTGTCTCTGCTTTCAGGCTTAACTGACATGACTCTTGTAGATGATGCAAGA 300
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DB 505 TCACATGCTCTTCTTCTGAGGACATATGAGGATGTCAAAATGCAATTTGGGCTC 564
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LOCUS
DEFINITION Sequence 39 from Patent WO0160849.
ACCESSION AX225029
VERSION AX225029.1 GI:15555102
KEYWORDS Equine influenza virus H3N8
SOURCE Equine influenza virus H3N8
ORGANISM Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
REFERENCE 1 Influenzavirus A.
AUTHORS Dowling, P.W. and Youngner, J.S.

TITLE Cold-adapted equine influenza viruses
JOURNAL Patent: WO 0160849-A 39 23-AUG-2001;
UNIV. OF PITTSBURGH OF THE COMMONWEALTH SYSTEM OF HIGHER EDUCATION (US)

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TITLE
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RESULT 14
AR455539
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 4.3e-191;
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RESULT 15
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 LOCUS
 DEFINITION Sequence 32 from Patent WO0160849. linear PAT 10-SEP-2001
 ACCESSION AX225022
 VERSION AX225022.1 GI:15555095
 KEYWORDS Equine influenza virus H3N8
 SOURCE Equine influenza virus H3N8
 ORGANISM Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenzavirus A.

REFERENCE
 1 Dowling, P.W. and Youngner, J.S.
 TITLE Cold-adapted equine influenza viruses
 JOURNAL Patent: WO 0160849-A 32 23-AUG-2001;
 UNIV. OF PITTSBURGH OF THE COMMONWEALTH SYSTEM OF HIGHER EDUCATION (US)

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ORIGIN
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 Best Local Similarity 100.0%; Pred No. 4.3e-191; Mismatches 0; Indels 0; Gaps 0;
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

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SUMMARIES

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2	82	7.0	313	7 US-11-087-099-3833	Sequence 3833, Ap
3	79.5	6.7	1115	7 US-11-087-099-8680	Sequence 8680, Ap
4	75.5	6.4	818	7 US-11-087-099-12309	Sequence 12309, A
5	75.5	6.4	2671	6 US-10-876-787-6	Sequence 6, Appli
6	75	6.4	784	6 US-10-873-528-36	Sequence 36, Appl
7	74	6.3	485	7 US-11-087-099-9751	Sequence 9751, Ap
8	74	6.3	509	7 US-11-072-512-2447	Sequence 2447, Ap
9	74	6.3	589	6 US-10-821-234-1494	Sequence 1494, Ap
10	73.5	6.2	943	6 US-10-467-657-5508	Sequence 5508, Ap
11	73.5	6.2	1037	7 US-11-052-554A-250	Sequence 250, App
12	73.5	6.2	1372	7 US-11-087-099-3054	Sequence 3054, Ap
13	73	6.2	468	7 US-11-124-367A-474	Sequence 474, App
14	73	6.2	821	7 US-11-124-367A-473	Sequence 473, App
15	72.5	6.2	427	6 US-10-467-657-4384	Sequence 4384, Ap
16	72.5	6.2	1674	7 US-11-231-599-55	Sequence 55, Appl
17	72	6.1	917	7 US-11-169-041-145	Sequence 145, App
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19	71.5	6.1	208	6 US-10-467-657-5842	Sequence 5842, Ap
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21	71.5	6.1	311	7 US-11-229-371-5	Sequence 5, Appli
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ALIGNMENTS

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; Sequence 5013, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 5013
; LENGTH: 1035
; TYPE: PRT
; ORGANISM: Pichia pastoris
US-11-087-099-5013

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QY	127	NIILKANFSVIFERLETILLRAFTEGA	155
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; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3833
; LENGTH: 313
; TYPE: PRT

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Sequence 245, App
Sequence 2, Appli
Sequence 2866, Ap
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Sequence 10561, A
Sequence 32, Appl
Sequence 58, Appl
Sequence 1567, Ap
Sequence 76, Appl
Sequence 4295, Ap
Sequence 9424, Ap
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Sequence 10149, A
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; Publication No. US20060041961A1
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; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
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; ORGANISM: Ipomoea nil
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; Publication No. US20060041961A1
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; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
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; CURRENT FILING DATE: 2005-03-22
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; LENGTH: 818
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; ORGANISM: Agrobacterium tumefaciens
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; Sequence 6, Application US/10876787
; Publication No. US20050287535A1
; GENERAL INFORMATION:
; APPLICANT: McGraith, Kevin P.
; APPLICANT: Kimberly-Clark worldwide, Inc.
; TITLE OF INVENTION: BIOMARKERS FOR WOUND HEALING
; FILE REFERENCE: 1443.156U51
; CURRENT APPLICATION NUMBER: US/10/876,787
; CURRENT FILING DATE: 2004-06-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 2671
; TYPE: PRT
; ORGANISM: Homo sapiens
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Matches 48; Conservative 30; Mismatches 70; Indels 63; Gaps 10;
QY 17 HVKRFADQE-----LGDAPFLDRRLRDQSLKGR-----GSTLGLDDETAT 58
DB 1790 HDKMKRQQETKSTVAVNNDLGSQPHEDREFVD-PTTKGRVASFSIFGSSRYSLGPSL 1848
QY 59 RAGKQIVQILEESDEALKMTIASVPASRYLTDMLDEMSRDWFMLMPKQKVTGSLCIR 118
DB 1849 RKGEHVSERV---QSSEMTGTVLIMQPLRLPL-OLLCENHNRD-----1887
QY 119 MDQAIMDKNIIKANFSVIFERLETLILLRAFTTEGAVVGEISPLPSLPGHTNEDVKNAI 178
DB 1888 LQNFILRCQN--NKTNYNLVCTLOPLDIMCGSTTGG-----LGLLGLYINED---NV 1934
QY 179 GVLIGGLKNDNTVRISETLORFAWRSSHEN 209
DB 1935 GLVITQL-----ETLTYEQCPCHEN 1955
RESULT 6
US-10-873-528-36
```

```
; Sequence 36, Application US/10873528
; Publication No. US20050276814A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129WO
; CURRENT APPLICATION NUMBER: US/10/873,528
; CURRENT FILING DATE: 2004-06-23
; PRIOR FILING DATE: 2004-06-23
; PRIOR FILING DATE: 2001-01-26
; PRIOR FILING DATE: 1998-03-27
; PRIOR FILING DATE: 1998-03-27
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 36
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-873-528-36

Query Match      6.4%; Score 75; DB 6; Length 784;
Best Local Similarity 22.6%; Pred. No. 22;
Matches 47; Conservative 30; Mismatches 71; Indels 60; Gaps 9;

QY 1 MDSNTVSPQVDCFLMVRKRFADQELG---DAPFLDRDRDQSLKGRSTLGLDIETA 57
DB 102 IDGDTVEV-----VIKQVADRNGTAAEAKIIDILEHSLTTVVGQ---IVLDDQKP 149

QY 58 TRAG-----KQIVEQ-----ILEESDEALKMTIASVPASRYLTDMLDMSRDWFL 105
DB 150 KYAGYRSKQKISQIYVVKPKLEGTEVLKVIDYPSKKH-----DFFVA 198

QY 106 MPKQKVTGSLCIRMDQAIMDKNIILKANFSVIFERLETLILLRAFTTEGAVVGEISPLPS 165
DB 199 SVLDVVGHSVDGID-----VLEVESMDIVSEFPE--AVVKEAESVDP 240

QY 166 LPQHTNE-----DVKNAGVLIGGLKWN 189
DB 241 APSQXDMEGRLDRDEITFTIDGADAKD 268

RESULT 7
US-11-087-099-9751
; Sequence 9751, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9751
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Glycine max
US-11-087-099-9751

Query Match      6.3%; Score 74; DB 7; Length 485;
Best Local Similarity 19.8%; Pred. No. 14;
Matches 49; Conservative 42; Mismatches 99; Indels 58; Gaps 12;

QY 8 SPQVDCFLMH-----VRKRFADQELGDAPFLDRRDQ-----KSLKGRGSTLIG- 51
DB 4 AFQKSWIEHTDLSVESMMLDNSAD---LDKEERPEVLSLLPPYEGKSVVLEGAGIGR 60

QY 52 LDLETRAGKQIVGEIILEE--ESDEAL-----KMTIASVPA-SRYLTDMLDMSRD 101
DB 61 FTVELAKKAGQLAVDPFTESAIKKNESINGHHKVKFCADVTSPNLIYSEGSVDLIIFSN 120
```

```
QY 102 WFMLMPKOKVTSGLCIRMDQAIMDKNIILKANFSVIFERLETLILLRAFTTEGAVVGEIS 161
DB 121 WLLMYLSDKEVENLAARMIK-----WLKVGGVVFFRE-----SCFHQSGDSKRYN 166
QY 162 PL-----PSL-----PCHTNEDEVKNAIGVLIGGLKWNNDTVRISETLQRFAP-----RSS 206
DB 167 PTHYREPRFYTKVFKCHECHISDDTRNSFELSLVGCKICAYVRNKNQNOICWLWKVRSQ 226
QY 207 HENGRRPSF 214
DB 227 DDRGFQRF 234

RESULT 8
US-11-072-512-2447
; Sequence 2447, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI TAKAO
; APPLICANT: SUGIYAMA TOMOYASU
; APPLICANT: OTSUKI TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR FILING DATE: 2005-03-07
; PRIOR FILING DATE: 2002-01-25
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2447
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2447

Query Match      6.3%; Score 74; DB 7; Length 509;
Best Local Similarity 23.3%; Pred. No. 15;
Matches 47; Conservative 27; Mismatches 78; Indels 50; Gaps 10;

QY 20 KRFADQELGD-----APFLDRDRDQSLKGRSTLGLDIETATRAGKQIV 65
DB 102 RRAAASKLGEFAKVLDELNVKSEIIPMFNSLASDEQD-----SVRLLAVEACVN-----I 151
QY 66 EQILEESDEALKMTIASVPASRYLTDMLDMSRDWFLMPK-----QKVTGSLCIRMDQ 121
DB 152 AQLLPQDEALVN-----PTLRQAAE---DKSVRVRYMVADKFTBLQKAVGPEITKTDL 203
QY 122 AAMDKNITILKANFSV-----IFERLETLILLRAFTTEGAVVGEISPL-LPSLPQHTNE 173
DB 204 VFAPQNLKDCAEVRAAASHKVGEFCEN---LSDACRENVIMSQLPCIKELVSDANQH 260
QY 174 VKNAIGVLIGGLK---WNNDTV 192
DB 261 VKSALASVIMGLSPILGKONTI 282
```

```

RESULT 9
US-10-821-234-1494
; Sequence 1494, Application US/10821234
; Publication No. US200502551141
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PC_SEQ_genes Version 1.0
; SEQ ID NO 1494
; LENGTH: 589
; TYPE: PRN
; ORGANISM: Homo sapiens
US-10-821-234-1494

Query Match
Best Local Similarity 6.3%; Score 74; DB 6; Length 589;
Matches 47; Conservative 27; Mismatches 78; Indels 50; Gaps 10;

QY 20 KRPADQELG-----APFLRLRRDQKSLKRGSTGLGLDIETATRAGQIV 65
DB 182 RRAAASKLGEFAKVLDELNVKSEIIPFNSNLASDEQ-----SVRLLAVEACVN-----I 231
QY 66 EQILEESDEALKMTIASVPASRYLTDMTLDEMSRDFMLMPK---QKVTGSLCIRMDQ 121
DB 232 AOLLPQEDLEALVM-----PTLRQAAE---DKSWRVRYMVADKFTBLQKAVGPEITKIDL 283
QY 122 AIMDKNIILKANFSV-----IFERLETLILLRAFTTEGAVVGEISP-LPSLPQHTNED 173
DB 284 VPAFQNLAKMCEAEVRAAASHKVKFCEN---LSADCRENVIMSQILPCIKELVSDANQH 340
QY 174 VKNAIGVLIGLK---WNDNTV 192
DB 341 VKSALASVIMGLSPILGKDNTI 362

RESULT 10
US-10-467-657-5508
; Sequence 5508, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA, Maria Rita
; APPLICANT: PIZZA, Mariagrazia
; APPLICANT: MASIGNANI, Vega
; APPLICANT: MONACI, Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5508
; LENGTH: 943
; TYPE: PRN
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5508

Query Match
Best Local Similarity 6.2%; Score 73.5; DB 6; Length 943;
Matches 39; Conservative 29; Mismatches 58; Indels 43; Gaps 8;

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QY 34 DRLRRDQ-----KSLKRGSTGLGLDIETATRAGQIVQILEESDEALKMTIASVPASRY 89
DB 299 DRRNRDDEGQGRNAKGGAKGGRDRNNAINGCD---ERVGGKGGKGLKLE-PNQHAFQA 354
QY 90 LTDMTLDEMSRDFMLMPKQKVTGSLC-----IRMDQAIMDKNIILKANFSVIPERLE 142
DB 355 PTEPVVHE-----VLVPETITVADLAHKMAVGVEMVKALMKGMVVTINOSI---QDQT 406
QY 143 TLILLR-----AFTERGAVVGEISPLPSLP-----GHTN 171
DB 407 ALIVVKKLGHGKPRAADPEAFLEGGAEEAEALPRPVVTVNGHYD 455

RESULT 11
US-11-052-554A-250
; Sequence 250, Application US/11052554A
; Publication No. US20050288666A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 250
; LENGTH: 1037
; TYPE: PRN
; ORGANISM: Neisseria meningitidis 22491
US-11-052-554A-250

Query Match
Best Local Similarity 6.2%; Score 73.5; DB 7; Length 1037;
Matches 51; Conservative 32; Mismatches 70; Indels 63; Gaps 12;

QY 16 WHVKRRF-ADQELGDAPFLDLRLRRDQKSLKRGSTL-----GL-----DIETA 57
DB 760 WTVRTIFQGTKPITSAPAIQSKDKRVVIFGTGSDLSDEDDVLSTDEQHIYGPNDNTNTG 819
QY 58 TR---AGKQIVQILEESDEALKMTIASVPASRYLTDMTLDEMSRD---WFM-LMPKQKV 111
DB 820 TAQELGKGLLEQKLEEN-----KTLFLTDYKRSDDSGDKGVVVKLQKQKV 867
QY 112 TGSLCIRMDQAIMDKNIILKANFSVIFE-----RLETLILLRAFTTEGAVVGEISPLP 164
DB 868 T-----VKPTVLRFAFTVTHKYTGNDKCGAETAL-LGINTADGKGLTKKSARP 915
QY 165 SLPGHTNE-----DVQNAIG---VLIGLKNWNTV 192
DB 916 IVPAAANSKVAQYSGDKKTSSTSGKSPIGOMKDGTV 951

RESULT 12
US-11-087-099-3054
; Sequence 3054, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3054
; LENGTH: 1372
; TYPE: PRN
; ORGANISM: Cercospora zeae-maydis
US-11-087-099-3054

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Db 228 KLKWA---DRLPRILY--YKQEGEIVSRDDPQGRVSIIDRLP-----QASSRWVAIGR 277

Oy 185 LKWNNTVRI-----SETLQRFAPWRSSHENGREPF 214

Db 278 LDINTSGLLILTTSGELVQRF-----HPSF 303

Search completed: March 7, 2006, 19:26:00
Job time : 21 secs

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OM protein - protein search, using sw model

Run on: March 7, 2006, 19:22:04 ; Search time 166 Seconds
(without alignments)
578.920 Million cell updates/sec

Title: US-10-734-373-58
Perfect score: 1178
Sequence: 1 MDSNTVSSFDVDFLWVHK.....RPSFPKOKRMERTIEPEV 230

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*

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2: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1178	100.0	230	4	US-10-065-133A-51
2	1178	100.0	230	4	US-10-065-133A-58
3	1178	100.0	230	4	US-10-734-373-51
4	1178	100.0	230	4	US-10-734-373-58
5	1178	100.0	230	5	US-10-181-585B-33
6	1178	100.0	230	5	US-10-181-585B-40
7	1061	90.1	238	5	US-10-654-737-3
8	1055	89.6	237	4	US-10-381-530-17
9	1052	89.3	230	5	US-10-654-737-5
10	488	41.4	97	4	US-10-065-133A-55
11	488	41.4	97	4	US-10-734-373-55
12	488	41.4	97	5	US-10-181-585B-37
13	400	34.0	344	3	US-09-822-927-973
14	400	34.0	344	3	US-09-895-793-973
15	387	32.9	312	4	US-10-312-089-1
16	385.5	32.7	312	4	US-10-312-089-3
17	385	32.7	282	4	US-10-226-872-10
18	385	32.7	282	4	US-10-473-127-1114
19	384	32.6	403	5	US-10-650-608-10
20	100	8.5	478	4	US-10-369-493-501
21	93	7.9	477	4	US-10-369-493-21219
22	93	7.9	1873	4	US-10-087-192-666
23	90	7.6	233	4	US-10-424-599-213467
24	89.5	7.6	996	5	US-10-719-993-597
25	89.5	7.6	1876	3	US-09-839-479-70
26	89.5	7.6	1876	4	US-10-376-537-71
27	89.5	7.6	1876	4	US-10-702-148-70

28	89	7.6	1448	4	US-10-282-122A-66468	Sequence 66468, A
29	87.5	7.4	842	4	US-10-820-307-3	Sequence 3, Appli
30	87.5	7.4	844	3	US-09-866-020-30	Sequence 30, Appl
31	87.5	7.4	844	3	US-09-813-148-4	Sequence 4, Appli
32	87.5	7.4	844	3	US-09-810-796-14	Sequence 14, Appl
33	87.5	7.4	844	4	US-10-295-027-282	Sequence 282, App
34	87.5	7.4	844	4	US-10-661-629-4	Sequence 4, Appli
35	87.5	7.4	844	5	US-10-643-795A-152	Sequence 152, App
36	87.5	7.4	844	5	US-10-850-928-34	Sequence 34, Appl
37	87.5	7.4	844	5	US-10-948-493-29	Sequence 29, Appl
38	87.5	7.4	844	5	US-10-948-518-152	Sequence 152, App
39	87.5	7.4	844	5	US-10-482-83A-161	Sequence 161, App
40	87.5	7.4	844	5	US-10-282-436A-601	Sequence 601, App
41	87.5	7.4	872	4	US-10-345-680-17	Sequence 17, Appli
42	87.5	7.4	872	4	US-10-096-578-2	Sequence 2, Appli
43	87.5	7.4	872	4	US-10-820-307-2	Sequence 7, Appli
44	87.5	7.4	872	4	US-10-744-796-7	Sequence 41003, A
45	87.5	7.4	912	5	US-10-450-763-41003	

ALIGNMENTS

RESULT 1
US-10-065-133A-51
; Sequence 51, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent version 3.1
; SEQ ID NO 51
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-51

Query Match 100.0%; Score 1178; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 4.1e-116;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MDSNTVSSFDVDFLWVHKRFADQELGDAPFLDLRRDQKSLKRGSTGLDIETATRA	60
DB	1	MDSNTVSSFDVDFLWVHKRFADQELGDAPFLDLRRDQKSLKRGSTGLDIETATRA	60
QY	61	GKQIVQEILEESDEALKMTIASVPASRYLTDMTIDMSRDWFMPLPKOKVTGSLCIRMD	120
DB	61	GKQIVQEILEESDEALKMTIASVPASRYLTDMTIDMSRDWFMPLPKOKVTGSLCIRMD	120
QY	121	QAIMDKNIILKANSVIFERLETLILRAFTTEGAVGVEISPLPSLPCHTNDVQNAIGV	180
DB	121	QAIMDKNIILKANSVIFERLETLILRAFTTEGAVGVEISPLPSLPCHTNDVQNAIGV	180
QY	181	LIGLKWNDNVTIRSETLQFAWRSSHENGSRPSFPKOKRMERTIEPEV	230
DB	181	LIGLKWNDNVTIRSETLQFAWRSSHENGSRPSFPKOKRMERTIEPEV	230

RESULT 2
US-10-065-133A-58
; Sequence 58, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.

```
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 59
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
; US-10-065-133A-58

Query Match      100.0%; Score 1178; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 4, 1e-116;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDSNTVSSFOVDCFLWHVRKGFADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60
Db 1 MDSNTVSSFOVDCFLWHVRKGFADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60

Qy 61 GKQIVEQILLESDEALKMTIASVPASRYLTDMTLDMSRDWFMMPKQKVMERTIEPEV 120
Db 61 GKQIVEQILLESDEALKMTIASVPASRYLTDMTLDMSRDWFMMPKQKVMERTIEPEV 120

Qy 121 QAIMDKNIILKANFSVIFERLETLILLRAFTBEGAVGGEISPLSPGHTNEDVKNAIGV 180
Db 121 QAIMDKNIILKANFSVIFERLETLILLRAFTBEGAVGGEISPLSPGHTNEDVKNAIGV 180

Qy 181 LIGGLKWNNDTVRISETLQRFAMRSSHENGSRFPFPKQKRMERTIEPEV 230
Db 181 LIGGLKWNNDTVRISETLQRFAMRSSHENGSRFPFPKQKRMERTIEPEV 230
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```
RESULT 3
US-10-734-373-51
; Sequence 51, Application US/10734373
; Publication No. US20040137015A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/734,373
; PRIOR FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
; US-10-734-373-51

Query Match      100.0%; Score 1178; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 4, 1e-116;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDSNTVSSFOVDCFLWHVRKGFADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60
Db 1 MDSNTVSSFOVDCFLWHVRKGFADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60

Qy 61 GKQIVEQILLESDEALKMTIASVPASRYLTDMTLDMSRDWFMMPKQKVMERTIEPEV 120
Db 61 GKQIVEQILLESDEALKMTIASVPASRYLTDMTLDMSRDWFMMPKQKVMERTIEPEV 120
```

```
Qy 121 QAIMDKNIILKANFSVIFERLETLILLRAFTBEGAVGGEISPLSPGHTNEDVKNAIGV 180
Db 121 QAIMDKNIILKANFSVIFERLETLILLRAFTBEGAVGGEISPLSPGHTNEDVKNAIGV 180

Qy 181 LIGGLKWNNDTVRISETLQRFAMRSSHENGSRFPFPKQKRMERTIEPEV 230
Db 181 LIGGLKWNNDTVRISETLQRFAMRSSHENGSRFPFPKQKRMERTIEPEV 230

RESULT 4
US-10-734-373-58
; Sequence 58, Application US/10734373
; Publication No. US20040137015A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/734,373
; PRIOR FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
; US-10-734-373-58

Query Match      100.0%; Score 1178; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 4, 1e-116;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDSNTVSSFOVDCFLWHVRKGFADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60
Db 1 MDSNTVSSFOVDCFLWHVRKGFADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60

Qy 61 GKQIVEQILLESDEALKMTIASVPASRYLTDMTLDMSRDWFMMPKQKVMERTIEPEV 120
Db 61 GKQIVEQILLESDEALKMTIASVPASRYLTDMTLDMSRDWFMMPKQKVMERTIEPEV 120

Qy 121 QAIMDKNIILKANFSVIFERLETLILLRAFTBEGAVGGEISPLSPGHTNEDVKNAIGV 180
Db 121 QAIMDKNIILKANFSVIFERLETLILLRAFTBEGAVGGEISPLSPGHTNEDVKNAIGV 180

Qy 181 LIGGLKWNNDTVRISETLQRFAMRSSHENGSRFPFPKQKRMERTIEPEV 230
Db 181 LIGGLKWNNDTVRISETLQRFAMRSSHENGSRFPFPKQKRMERTIEPEV 230
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RESULT 5
US-10-181-585B-33
; Sequence 33, Application US/10181585B
; Publication No. US20050175985A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System
; APPLICANT: of Higher Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C3-PUS
; CURRENT APPLICATION NUMBER: US/10/181,585B
; CURRENT FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: PCT/US01/05048
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/506,286
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
```

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; LENGTH: 230
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-10-181-585B-33

Query Match 100.0%; Score 1178; DB 5; Length 230;
Best Local Similarity 100.0%; Pred. No. 4.1e-116;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSNTVSSFOVDCFLMHWKRPADQELGDAPFLDLRLRRDQKSLKGRGSLGLDIETATRA 60
DB 1 MDSNTVSSFOVDCFLMHWKRPADQELGDAPFLDLRLRRDQKSLKGRGSLGLDIETATRA 60
QY 61 GKQIVEQILEESDEALKMTIASVPASRYLDTMTLDEMSSDFWMLMPKQKVTGSLCIRMD 120
DB 61 GKQIVEQILEESDEALKMTIASVPASRYLDTMTLDEMSSDFWMLMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTERGAVVGEISPLPSLPGHTNEDVKNAIGV 180
DB 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTERGAVVGEISPLPSLPGHTNEDVKNAIGV 180
QY 181 LIGGLKWNNTVRISETLQRFARWSSHENGSRPSPFPKQKRWERTIEPEV 230
DB 181 LIGGLKWNNTVRISETLQRFARWSSHENGSRPSPFPKQKRWERTIEPEV 230

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RESULT 6

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US-10-181-585B-40
; Sequence 40, Application US/10181585B
; Publication No. US20050175985A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System
; APPLICANT: of Higher Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C3-PUS
; CURRENT APPLICATION NUMBER: US/10/181.585B
; PRIOR FILING DATE: 2003-12-08
; PRIOR FILING DATE: PCT/US01/05048
; PRIOR FILING DATE: 2001-02-16
; PRIOR FILING DATE: 09/506,286
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 40
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-10-181-585B-40

Query Match 100.0%; Score 1178; DB 5; Length 230;
Best Local Similarity 100.0%; Pred. No. 4.1e-116;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSNTVSSFOVDCFLMHWKRPADQELGDAPFLDLRLRRDQKSLKGRGSLGLDIETATRA 60
DB 1 MDSNTVSSFOVDCFLMHWKRPADQELGDAPFLDLRLRRDQKSLKGRGSLGLDIETATRA 60
QY 61 GKQIVEQILEESDEALKMTIASVPASRYLDTMTLDEMSSDFWMLMPKQKVTGSLCIRMD 120
DB 61 GKQIVEQILEESDEALKMTIASVPASRYLDTMTLDEMSSDFWMLMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTERGAVVGEISPLPSLPGHTNEDVKNAIGV 180
DB 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTERGAVVGEISPLPSLPGHTNEDVKNAIGV 180
QY 181 LIGGLKWNNTVRISETLQRFARWSSHENGSRPSPFPKQKRWERTIEPEV 230
DB 181 LIGGLKWNNTVRISETLQRFARWSSHENGSRPSPFPKQKRWERTIEPEV 230

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RESULT 7

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US-10-654-737-3
; Sequence 3, Application US/10654737
; Publication No. US20050054846A1
; GENERAL INFORMATION:
; APPLICANT: St. Jude Children's Research Hospital
; APPLICANT: Webster, Robert G
; APPLICANT: Webby, Richard J
; APPLICANT: Ozaki, Hiroichi
; TITLE OF INVENTION: Improved Method for Generating Influenza Viruses and Vaccines
; FILE REFERENCE: SJ-02-0016
; CURRENT APPLICATION NUMBER: US/10/654,737
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 3
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Influenza A virus
US-10-654-737-3

Query Match 90.1%; Score 1061; DB 5; Length 238;
Best Local Similarity 88.7%; Pred. No. 1.1e-103;
Matches 204; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

QY 1 MDSNTVSSFOVDCFLMHWKRPADQELGDAPFLDLRLRRDQKSLKGRGSLGLDIETATRA 60
DB 1 MDSNTVSSFOVDCFLMHWKRPADQELGDAPFLDLRLRRDQKSLKGRGSLGLDIETATRA 60
QY 61 GKQIVEQILEESDEALKMTIASVPASRYLDTMTLDEMSSDFWMLMPKQKVTGSLCIRMD 120
DB 61 GKQIVEQILEESDEALKMTIASVPASRYLDTMTLDEMSSDFWMLMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTERGAVVGEISPLPSLPGHTNEDVKNAIGV 180
DB 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTERGAVVGEISPLPSLPGHTNEDVKNAIGV 180
QY 181 LIGGLKWNNTVRISETLQRFARWSSHENGSRPSPFPKQKRWERTIEPEV 230
DB 181 LIGGLKWNNTVRISETLQRFARWSSHENGSRPSPFPKQKRWERTIEPEV 230

RESULT 8
US-10-381-530-17
; Sequence 17, Application US/10381530
; Publication No. US20040137013A1
; GENERAL INFORMATION:
; APPLICANT: KATINGER, Hermann
; APPLICANT: EGOROV, Andre
; APPLICANT: FERKO, Boris
; APPLICANT: ROMANOVA, Julia
; APPLICANT: KATINGER, Dietmar
; TITLE OF INVENTION: LIVE VACCINE AND METHOD OF MANUFACTURE
; FILE REFERENCE: P/167-134
; CURRENT APPLICATION NUMBER: US/10/381,530
; CURRENT FILING DATE: 2003-11-24
; PRIOR FILING DATE: PCT/EP01/11087
; PRIOR FILING DATE: 2001-09-25
; PRIOR FILING DATE: 00120896.6
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 17
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Influenza virus A/Singapore/1/57/ca
US-10-381-530-17

Query Match 89.6%; Score 1055; DB 4; Length 237;
Best Local Similarity 87.8%; Pred. No. 4.7e-103;
Matches 202; Conservative 17; Mismatches 11; Indels 0; Gaps 0;

QY 1 MDSNTVSSFOVDCFLMHWKRPADQELGDAPFLDLRLRRDQKSLKGRGSLGLDIETATRA 60

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Db 1 MDNVTSSFOVDCFLMHWKQVADQELGDPFLDLRLRQKSLRGSTLGINIETATRV 60
Qy 61 GKQIVEOILLESDEALKMTIASVPASRYLTDMTLDMSRDWFMKPKKVTGSLCIRMD 120
Db 61 GKQIVERILKESDEALKMTIASVPASRYLTDMTLDMSRDWFMKPKKVTGSLCIRMD 120
Qy 121 QAIMDKNIIKANFSVIPERLETLILLRAFTTEGAVGVEISPLPSLPGHTNEDVKNAGV 180
Db 121 QAIMDKNIIKANFSVIPERLETLILLRAFTTEGAVGVEISPLPSLPGHTNEDVKNAGV 180
Qy 181 LIGGLKWNNDTVRISETLQRFAPWRSSHENGSRPSPPKPKKRMERTIEPEV 230
Db 181 LIGGLEWNNNTVRVSKTLQRFAPWRSSHENGSRPSPPKPKKRMERTIRSKV 230

RESULT 9
US-10-654-737-5
; Sequence 55, Application US/10654737
; Publication No. US20050054846A1
; GENERAL INFORMATION:
; APPLICANT: St. Jude Children's Research Hospital
; APPLICANT: Webster, Robert G
; APPLICANT: Webby, Richard J
; APPLICANT: Ozaki, Hiroichi
; TITLE OF INVENTION: Improved Method for Generating Influenza Viruses and Vaccines
; FILE REFERENCE: SJ-02-0016
; CURRENT APPLICATION NUMBER: US/10/654,737
; CURRENT FILING DATE: 2003-09-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Influenza A virus
US-10-654-737-5

Query Match 89.3%; Score 1052; DB 5; Length 230;
Best Local Similarity 87.8%; Pred. No. 9.3e-103; Indels 0; Gaps 0;
Matches 202; Conservative 16; Mismatches 12;

Qy 1 MDNVTSSFOVDCFLMHWKQVADQELGDPFLDLRLRQKSLRGSTLGINIETATRA 60
Db 1 MDNVTSSFOVDCFLMHWKQVADQELGDPFLDLRLRQKSLRGSTLGINIETATRA 60
Qy 61 GKQIVEOILLESDEALKMTIASVPASRYLTDMTLDMSRDWFMKPKKVTGSLCIRMD 120
Db 61 GKQIVERILKESDEALKMTIASVPASRYLTDMTLDMSRDWFMKPKKVTGSLCIRMD 120
Qy 121 QAIMDKNIIKANFSVIPERLETLILLRAFTTEGAVGVEISPLPSLPGHTNEDVKNAGV 180
Db 121 QAIMDKNIIKANFSVIPERLETLILLRAFTTEGAVGVEISPLPSLPGHTNEDVKNAGV 180
Qy 181 LIGGLKWNNDTVRISETLQRFAPWRSSHENGSRPSPPKPKKRMERTIEPEV 230
Db 181 LIGGLEWNNNTVRVSKTLQRFAPWRSSHENGSRPSPPKPKKRMERTIRSEV 230

RESULT 10
US-10-065-133A-55
; Sequence 55, Application US/10065133A
; Publication No. US20030199074A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; CURRENT APPLICATION NUMBER: US/10/065,133A
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 97
; ORGANISM: Equine influenza virus H3N8
US-10-734-373-55

Query Match 41.4%; Score 488; DB 4; Length 97;
Best Local Similarity 99.0%; Pred. No. 1.17e-43;
Matches 96; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 134 FSVIFERLETLILLRAFTTEGAVGVEISPLPSLPGHTNEDVKNAGVILGGLKWNNDTVR 193
Db 1 FSVIFERLETLILLRAFTTEGAVGVEISPLPSLPGHTNEDVKNAGVILGGLKWNNDTVR 60
Qy 194 ISETLQRFAPWRSSHENGSRPSPPKPKKRMERTIEPEV 230
Db 61 ISETLQRFAPWRSSHENGSRPSPPKPKKRMERTIEPEV 97

RESULT 11
US-10-734-373-55
; Sequence 55, Application US/10734373
; Publication No. US20040137015A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EO-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/734,373
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 09/133,921
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 97
; ORGANISM: Equine influenza virus H3N8
US-10-734-373-55

Query Match 41.4%; Score 488; DB 4; Length 97;
Best Local Similarity 99.0%; Pred. No. 1.17e-43;
Matches 96; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 134 FSVIFERLETLILLRAFTTEGAVGVEISPLPSLPGHTNEDVKNAGVILGGLKWNNDTVR 193
Db 1 FSVIFERLETLILLRAFTTEGAVGVEISPLPSLPGHTNEDVKNAGVILGGLKWNNDTVR 60
Qy 194 ISETLQRFAPWRSSHENGSRPSPPKPKKRMERTIEPEV 230
Db 61 ISETLQRFAPWRSSHENGSRPSPPKPKKRMERTIEPEV 97

RESULT 12
US-10-181-585B-37
; Sequence 37, Application US/10181585B
; Publication No. US20050175985A1
; GENERAL INFORMATION:
; APPLICANT: The University of Pittsburgh - of the Commonwealth System
; APPLICANT: of Higher Education
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EO-1-C3-PUS
; CURRENT APPLICATION NUMBER: US/10/181,585B
; CURRENT FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: PCT/US01/05048
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/506,286
; PRIOR FILING DATE: 2000-02-16
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NUMBER OF SEQ ID NOS: 130
SOFTWARE: Patent in version 3.2
SEQ ID NO 37
LENGTH: 97
TYPE: PRT
ORGANISM: Equine influenza virus H3N8
US-10-181-585B-37

Query Match 41.4%; Score 488; DB 5; Length 97;
Best Local Similarity 99.0%; Pred. No. 1.7e-43;
Matches 96; Conservative 1; Indels 0; Gaps 0;
QY 134 PSVIFERLETLILLRAFTGEGAVGEISPLPSLPGHTNEDVKNALGVILGLKWNNTVR 193
DB 1 PSVIFERLETLILLRAFTGEGAVGEISPLPSLPGHTNEDVKNALGVILGLKWNNTVR 60
QY 194 ISETLQFARSSHENGREPSPPKQKXWERTIEPV 230
DB 61 ISETLQFARSSHENGREPSPPKQKXWERTIEPV 97

RESULT 13
US-09-822-827-973
Sequence 973; Application US/09822827
Patent No. US20020081680A1

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822.827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 973
LENGTH: 344
TYPE: PRT
ORGANISM: Homo sapiens
US-09-822-827-973

Query Match 34.0%; Score 400; DB 3; Length 344;
Best Local Similarity 73.5%; Pred. No. 2.2e-33;
Matches 86; Conservative 8; Mismatches 15; Indels 8; Gaps 2;
QY 1 MDSNTVSSFOVDCFLMHWKRFADQELGDAPFLDLRLRRDQKSLKGRGSLGLDIETATRA 60
DB 1 MDPNTVSSFOVDCFLMHWKRFADQELGDAPFLDLRLRRDQKSLKGRGSLGLDIETATRA 60
QY 61 GKQIVEQILEESDEALKMTIASVPASRYLTD-----MTLDEMSEDFWMLMPKQKVT 112
DB 61 GKQIVERILKEESDEALKMTIAS-----EEFLTPKKLQCVDLHVISNDVCAQVHPQKVT 114

RESULT 14
US-09-895-793-973
Sequence 973; Application US/09895793
Publication No. US20020192763A1

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Rasir A.W.
APPLICANT: Hepler, William T.

APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895.793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 973
LENGTH: 344
TYPE: PRT
ORGANISM: Homo sapiens
US-09-895-793-973

Query Match 34.0%; Score 400; DB 3; Length 344;
Best Local Similarity 73.5%; Pred. No. 2.2e-33;
Matches 86; Conservative 8; Mismatches 15; Indels 8; Gaps 2;
QY 1 MDSNTVSSFOVDCFLMHWKRFADQELGDAPFLDLRLRRDQKSLKGRGSLGLDIETATRA 60
DB 1 MDPNTVSSFOVDCFLMHWKRFADQELGDAPFLDLRLRRDQKSLKGRGSLGLDIETATRA 60
QY 61 GKQIVEQILEESDEALKMTIASVPASRYLTD-----MTLDEMSEDFWMLMPKQKVT 112
DB 61 GKQIVERILKEESDEALKMTIAS-----EEFLTPKKLQCVDLHVISNDVCAQVHPQKVT 114

RESULT 15

US-10-312-089-1
Sequence 1; Application US/10312089
Publication No. US20030143240A1
GENERAL INFORMATION:
APPLICANT: Cabezon-Silva, Teresa Elisa Virginia
APPLICANT: Bernanne, Philippe Jean Gervais Chislain
TITLE OF INVENTION: Prostate Protein Vaccine Comprising
PERIVASCULAR THIOLESTEROL RESIDUES AND METHODS FOR PRODUCING SAID
TITLE OF INVENTION: Perivascular Thiol Residues and Methods for Producing Said
TITLE OF INVENTION: Antigen
FILE REFERENCE: 945224
CURRENT APPLICATION NUMBER: US/10/312.089
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: PCT/EP01/07082
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: GB 0015722.2
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 312
TYPE: PRT
ORGANISM: Homo sapien
US-10-312-089-1

Query Match 32.9%; Score 387; DB 4; Length 312;
Best Local Similarity 44.2%; Pred. No. 4.6e-32;
Matches 96; Conservative 24; Mismatches 55; Indels 42; Gaps 5;
QY 1 MDSNTVSSFOVDCFLMHWKRFADQELGDAPFLDLRLRRDQKSLKGRGSLGLDIETATRA 60
DB 1 MDPNTVSSFOVDCFLMHWKRFADQELGDAPFLDLRLRRDQKSLKGRGSLGLDIETATRA 60
QY 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMTLDEMSEDFWMLMPKQKVT 112
DB 61 GKQIVERILKEESDEALKMTIWDGDCSPH-----SOPWQAALWMENELFCSGVLVH 111
QY 107 PKQKVTGSLCTRMDOAI-----MDK-----NIIKANFSV-----IFERLETLILL 147
DB 112 POWLSAAACFQNSYTTIGLGLHSLDQEPQSQWSEASLSVRHPEYRNRELLANDMLIKL 171

Qy 148 RAFTTEGAVVGEISPLSPFGHTNEDVKNAGVLIIG 184
Db 172 DESVSESDTIRSISIASQCPAGNSCLVSGWGLLANG 208

Search completed: March 7, 2006, 19:25:33
Job time : 167 secs

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OM protein - protein search, using sw model

Run on: March 7, 2006, 19:21:19 ; Search time 47 seconds
(without alignments)
404.583 Million cell updates/sec

Title: US-10-734-373-58

Perfect score: 1178

Sequence: 1 MDSNTVSSFQVDCFLMHRK.....RPSFPKQKRMERTIEPV 230

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
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3: /cgn2_6/ptodata/1/iaa/H COMB.pap.*
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5: /cgn2_6/ptodata/1/iaa/RE COMB.pap.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1178	100.0	230	2	US-09-506-286B-51
2	1178	100.0	230	2	US-09-506-286B-58
3	1178	100.0	230	2	US-10-065-133A-51
4	1178	100.0	230	2	US-10-065-133A-58
5	1010	85.7	237	1	US-08-467-587A-4
6	488	41.4	97	2	US-09-506-286B-55
7	488	41.4	97	2	US-10-065-133A-55
8	392.5	33.3	306	4	PCT-US94-01149-10
9	390.5	33.1	337	1	US-08-441-857-8
10	390.5	33.1	337	2	US-08-193-159-8
11	390.5	33.1	337	2	US-09-283-646C-8
12	389.5	33.1	230	4	PCT-US94-01149-12
13	389.5	33.1	230	4	PCT-US94-01149-72
14	389.5	33.1	304	4	PCT-US94-01149-55
15	389.5	33.1	304	4	PCT-US94-01149-57
16	387.5	32.9	225	4	PCT-US94-01149-30
17	387.5	32.9	231	4	PCT-US94-01149-29
18	387.5	32.9	242	4	PCT-US94-01149-18
19	385.5	32.7	150	1	US-08-388-267C-4
20	385.5	32.7	150	2	US-09-277-720-4
21	385.5	32.7	338	1	US-08-441-857-12
22	385.5	32.7	338	2	US-08-193-159-12
23	385.5	32.7	338	2	US-09-283-646C-12
24	385	32.7	226	4	PCT-US94-01149-56
25	384	32.6	158	4	PCT-US94-01149-27
26	384	32.6	163	4	PCT-US94-01149-28
27	384	32.6	238	4	PCT-US94-01149-24

28	384	32.6	304	4	PCT-US94-01149-32	Sequence 32, Appl
29	384	32.6	307	4	PCT-US94-01149-16	Sequence 16, Appl
30	380	32.3	338	1	US-08-441-857-10	Sequence 10, Appl
31	380	32.3	338	2	US-08-193-159-10	Sequence 10, Appl
32	380	32.3	338	2	US-09-283-646C-10	Sequence 10, Appl
33	377.5	32.0	339	1	US-08-441-857-6	Sequence 6, Appl
34	377.5	32.0	339	2	US-08-193-159-6	Sequence 6, Appl
35	377.5	32.0	339	2	US-09-283-646C-6	Sequence 6, Appl
36	222	18.8	233	4	PCT-US94-01149-14	Sequence 14, Appl
37	215.5	18.3	209	4	PCT-US94-01149-22	Sequence 22, Appl
38	214	18.2	269	4	PCT-US94-01149-20	Sequence 20, Appl
39	89.5	7.6	1876	2	US-09-418-710-71	Sequence 71, Appl
40	89.5	7.6	1876	2	US-09-839-479-70	Sequence 70, Appl
41	87.5	7.4	844	2	US-09-813-148-4	Sequence 4, Appl
42	87.5	7.4	844	2	US-09-590-304-4	Sequence 4, Appl
43	87.5	7.4	844	2	US-09-492-361-34	Sequence 34, Appl
44	87.5	7.4	844	2	US-09-866-020A-29	Sequence 29, Appl
45	87.5	7.4	872	2	US-09-177-650-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-506-286B-51
; Sequence 51, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; APPLICANT: The University of Pittsburgh, of the Commonwealth
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; PRIOR FILING DATE: 2000-02-16
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 51
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-09-506-286B-51

Query Match		100.0%	Score 1178;	DB 2;	Length 230;
Best Local Similarity		100.0%	Pred. No. 2.1e-124;		
Matches 230;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MDSNTVSSFQVDCFLMHRKRFADQELGDAPFLDLRLRRDQKSLKGRGSLGLDIETATRA	60		
DB	1	MDSNTVSSFQVDCFLMHRKRFADQELGDAPFLDLRLRRDQKSLKGRGSLGLDIETATRA	60		
QY	61	GRQIVEQLEESDEALKMTIASVPASRYLTDMTLDEMSSDFMPLMPKQKVTGSLCIRMD	120		
DB	61	GRQIVEQLEESDEALKMTIASVPASRYLTDMTLDEMSSDFMPLMPKQKVTGSLCIRMD	120		
QY	121	QAIMDKNIILKANFSVIFERLETLILLRAFTTEGAVVGEISPLSPGHNTEDVKNATGV	180		
DB	121	QAIMDKNIILKANFSVIFERLETLILLRAFTTEGAVVGEISPLSPGHNTEDVKNATGV	180		
QY	181	LIGGLKWNNTVRISETLQFAWRSHHENGRRSPPPKQKRMERTIEPV	230		
DB	181	LIGGLKWNNTVRISETLQFAWRSHHENGRRSPPPKQKRMERTIEPV	230		

RESULT 2

US-09-506-286B-58
; Sequence 58, Application US/09506286B
; Patent No. 6482414
; GENERAL INFORMATION:

```
; APPLICANT: Dowling, Patricia W.
; APPLICANT: Youngner, Julius S.
; TITLE OF INVENTION: The University of Pittsburgh, of the Commonwealth
; FILE REFERENCE: EQ-1-C2
; CURRENT APPLICATION NUMBER: US/09/506,286B
; CURRENT FILING DATE: 2000-02-16
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 58
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-10-065-286B-58

Query Match      100.0%; Score 1178; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 2.1e-124; Indels 0; Gaps 0;
Matches 230; Conservative 0; Mismatches 0;

Qy 1 MDSNTVSSFOVDCFLMHWKRFADQELGDPFLDLRRDQKSLKGRGSLGLDLETATRA 60
Db 1 MDSNTVSSFOVDCFLMHWKRFADQELGDPFLDLRRDQKSLKGRGSLGLDLETATRA 60
Qy 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMD 120
Db 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMD 120
Qy 121 QAIMDKNIILKANFVIFERLETLILLRAFTTEGAVVGEISPLSLPGHTNEDVKNAGV 180
Db 121 QAIMDKNIILKANFVIFERLETLILLRAFTTEGAVVGEISPLSLPGHTNEDVKNAGV 180
Qy 181 LIGGLKWNNDTVRISETLORFAWRSSHENGSRPSFPFKQKRWERTIEPEV 230
Db 181 LIGGLKWNNDTVRISETLORFAWRSSHENGSRPSFPFKQKRWERTIEPEV 230

Query Match      100.0%; Score 1178; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 2.1e-124; Indels 0; Gaps 0;
Matches 230; Conservative 0; Mismatches 0;

Qy 1 MDSNTVSSFOVDCFLMHWKRFADQELGDPFLDLRRDQKSLKGRGSLGLDLETATRA 60
Db 1 MDSNTVSSFOVDCFLMHWKRFADQELGDPFLDLRRDQKSLKGRGSLGLDLETATRA 60
Qy 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMD 120
Db 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMD 120
Qy 121 QAIMDKNIILKANFVIFERLETLILLRAFTTEGAVVGEISPLSLPGHTNEDVKNAGV 180
Db 121 QAIMDKNIILKANFVIFERLETLILLRAFTTEGAVVGEISPLSLPGHTNEDVKNAGV 180
Qy 181 LIGGLKWNNDTVRISETLORFAWRSSHENGSRPSFPFKQKRWERTIEPEV 230
Db 181 LIGGLKWNNDTVRISETLORFAWRSSHENGSRPSFPFKQKRWERTIEPEV 230

RESULT 3
US-10-065-133A-51
; Sequence 51, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 51
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-51

Query Match      100.0%; Score 1178; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 2.1e-124; Indels 0; Gaps 0;
Matches 230; Conservative 0; Mismatches 0;

Qy 1 MDSNTVSSFOVDCFLMHWKRFADQELGDPFLDLRRDQKSLKGRGSLGLDLETATRA 60
Db 1 MDSNTVSSFOVDCFLMHWKRFADQELGDPFLDLRRDQKSLKGRGSLGLDLETATRA 60
Qy 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMD 120
Db 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMD 120
Qy 121 QAIMDKNIILKANFVIFERLETLILLRAFTTEGAVVGEISPLSLPGHTNEDVKNAGV 180
Db 121 QAIMDKNIILKANFVIFERLETLILLRAFTTEGAVVGEISPLSLPGHTNEDVKNAGV 180
Qy 181 LIGGLKWNNDTVRISETLORFAWRSSHENGSRPSFPFKQKRWERTIEPEV 230
Db 181 LIGGLKWNNDTVRISETLORFAWRSSHENGSRPSFPFKQKRWERTIEPEV 230

RESULT 4
US-10-065-133A-58
; Sequence 58, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 58
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-58

Query Match      100.0%; Score 1178; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 2.1e-124; Indels 0; Gaps 0;
Matches 230; Conservative 0; Mismatches 0;

Qy 1 MDSNTVSSFOVDCFLMHWKRFADQELGDPFLDLRRDQKSLKGRGSLGLDLETATRA 60
Db 1 MDSNTVSSFOVDCFLMHWKRFADQELGDPFLDLRRDQKSLKGRGSLGLDLETATRA 60
Qy 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMD 120
Db 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMD 120
Qy 121 QAIMDKNIILKANFVIFERLETLILLRAFTTEGAVVGEISPLSLPGHTNEDVKNAGV 180
Db 121 QAIMDKNIILKANFVIFERLETLILLRAFTTEGAVVGEISPLSLPGHTNEDVKNAGV 180
Qy 181 LIGGLKWNNDTVRISETLORFAWRSSHENGSRPSFPFKQKRWERTIEPEV 230
Db 181 LIGGLKWNNDTVRISETLORFAWRSSHENGSRPSFPFKQKRWERTIEPEV 230

RESULT 5
US-10-065-133A-4
; Sequence 4, Application US/08467587A
; Patent No. 5843724
; GENERAL INFORMATION:
; APPLICANT: KRUG, ROBERT M.
; APPLICANT: QIAN, XIAO YAN
; TITLE OF INVENTION: CHIMERIC NUCLEIC ACIDS AND PROTEINS
; TITLE OF INVENTION: FOR INHIBITING HIV-1 EXPRESSION
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESS: Steinberg, Raekin & Davidson, P.C.
; STREET: 1140 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
```

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Db 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMD 120
Qy 121 QAIMDKNIILKANFVIFERLETLILLRAFTTEGAVVGEISPLSLPGHTNEDVKNAGV 180
Db 121 QAIMDKNIILKANFVIFERLETLILLRAFTTEGAVVGEISPLSLPGHTNEDVKNAGV 180
Qy 181 LIGGLKWNNDTVRISETLORFAWRSSHENGSRPSFPFKQKRWERTIEPEV 230
Db 181 LIGGLKWNNDTVRISETLORFAWRSSHENGSRPSFPFKQKRWERTIEPEV 230

RESULT 4
US-10-065-133A-58
; Sequence 58, Application US/10065133A
; Patent No. 6685946
; GENERAL INFORMATION:
; APPLICANT: Dowling, Patricia W.
; TITLE OF INVENTION: COLD-ADAPTED EQUINE INFLUENZA VIRUSES
; FILE REFERENCE: EQ-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/065,133A
; PRIOR FILING DATE: 2002-12-10
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: PCT/US99/18583
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 58
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Equine influenza virus H3N8
US-10-065-133A-58

Query Match      100.0%; Score 1178; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 2.1e-124; Indels 0; Gaps 0;
Matches 230; Conservative 0; Mismatches 0;

Qy 1 MDSNTVSSFOVDCFLMHWKRFADQELGDPFLDLRRDQKSLKGRGSLGLDLETATRA 60
Db 1 MDSNTVSSFOVDCFLMHWKRFADQELGDPFLDLRRDQKSLKGRGSLGLDLETATRA 60
Qy 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMD 120
Db 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMD 120
Qy 121 QAIMDKNIILKANFVIFERLETLILLRAFTTEGAVVGEISPLSLPGHTNEDVKNAGV 180
Db 121 QAIMDKNIILKANFVIFERLETLILLRAFTTEGAVVGEISPLSLPGHTNEDVKNAGV 180
Qy 181 LIGGLKWNNDTVRISETLORFAWRSSHENGSRPSFPFKQKRWERTIEPEV 230
Db 181 LIGGLKWNNDTVRISETLORFAWRSSHENGSRPSFPFKQKRWERTIEPEV 230

RESULT 5
US-08-467-587A-4
; Sequence 4, Application US/08467587A
; Patent No. 5843724
; GENERAL INFORMATION:
; APPLICANT: KRUG, ROBERT M.
; APPLICANT: QIAN, XIAO YAN
; TITLE OF INVENTION: CHIMERIC NUCLEIC ACIDS AND PROTEINS
; TITLE OF INVENTION: FOR INHIBITING HIV-1 EXPRESSION
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESS: Steinberg, Raekin & Davidson, P.C.
; STREET: 1140 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
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us-10-734-373-58.ra1

Wed Mar 8 09:11:19 2006

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;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 149,150
; FILING DATE: 05-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 013,415
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 108,914
; FILING DATE: 18-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 837,773
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 751,896
; FILING DATE: 30-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 387,200
; FILING DATE: 28-JUL-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 238,801
; FILING DATE: 02-NOV-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 645,732
; FILING DATE: 30-AUG-1984
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P50134 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-270-5096
; TELEFAX: 215-270-5090
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 306 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-01149-10

Query Match 33.3%; Score 392.5; DB 4; Length 306;
Best Local Similarity 47.8%; Pred. No. 1.2e-35;
Matches 100; Conservative 28; Mismatches 56; Indels 23; Gaps 8;

QY 1 MDSNTVSSFOVDCFLWHVYKRFADQELGDAFLLRLRRDQKSLKGRGSLGLDLETATRA 60
Db 1 MDPNTVSSFOVDCFLWHVYKRFADQELGDAFLLRLRRDQKSLKGRGSLGLDLETATRA 60
QY 61 GKQIVEQLKEESDEALKMTIASVPASRYLTDMTLDMSRDF-MLMPKQKVTGSL 115
Db 61 GKQIVERILKEESDEALKMTMGHGFAGIFENGWEGMIDGWYGFHQNSEGTOQA 120
QY 116 C-IRMDQAINDK-----NIIKANFSVIFERLETLILRAFTTEGAVVGEISPLSLPG 168
Db 121 ADLSTQAIDQINGKLNRFVIEKTEK--FHQIE-----KEFSE---VEGRIQDLKYVE 170
QY 169 HTNEDVKNAIGVLIGLKWNTVRISET 197
Db 171 DTKIDLSYNALLVALE-NQHTIDLDS 198

RESULT 9
US-08-441-857-8
; Sequence 8, Application US/08441857
; Patent No. 594236
; GENERAL INFORMATION:
; APPLICANT: SIMON, MARKUS
; APPLICANT: KRAMER, MICHAEL
; APPLICANT: SCHABBLE, ULRICH
; APPLICANT: WALLICH, REINHARD
; APPLICANT: LOBET, YVES
; TITLE OF INVENTION: OSP A PROTEINS OF BORRELIA BURGDORFERI SUBGROUPS, ENCODING GE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:

;
; ADDRESSEE: SMITHKLINE BEECHAM CORPORATION/CORPORATE INTELLECTUAL PROPERTY-UW
; STREET: P.O. BOX 1539
; CITY: KING OF PRUSSIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441.857
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/193,159
; FILING DATE: JULY 5, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: JEFFREY A. SUTTON
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: B45008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270 5024
; TELEFAX: (610) 270 5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 337 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: BORRELIA BURGDORFERI
; STRAIN: 19857
; IMMEDIATE SOURCE:
; CLONE: NS1-19857
; US-08-441-857-8

Query Match 33.1%; Score 390.5; DB 1; Length 337;
Best Local Similarity 42.4%; Pred. No. 2.3e-35;
Matches 112; Conservative 21; Mismatches 58; Indels 73; Gaps 10;

QY 1 MDSNTVSSFOVDCFLWHVYKRFADQELGDAFLLRLRRDQKSLKGRGSLGLDLETATRA 60
Db 1 MDPNTVSSFOVDCFLWHVYKRFADQELGDAFLLRLRRDQKSLKGRGSLGLDLETATRA 60
QY 61 GKQIVEQLKEESDEALKMTIASVPASRYLTDMTLDMSR-----DWFMLPKQKVTG 113
Db 61 GKQIVERILKEESDEALKMTMGKQNV-----SLDEKNSVSVDPGKMKVLSKKNKD 114
QY 114 SLICRMDQAINDKNIIILKA-----NFSVIFERLE-----TLILRAFTTEG 154
Db 115 G---KYDILMATVDNVDLKGTSKNGSGILEGVKADKSKVKLTVDADDLSKTTLVLEKDG 171
QY 155 AVV-----GEISPLSLPGH-----TWED-VKNAIGVLIGGL 185
Db 172 TVVSRKVTSKDKSTTEAKFNKSGELSEKMTFRANGTTLEYSQMTNEDNAKAVETLNKI 231
QY 186 KWNDN-----TVRISE---TLQR 200
Db 232 KFEGLASGKTAVEIKEGTVTLKR 255

RESULT 10
US-08-193-159-8
; Sequence 8, Application US/08193159
; Patent No. 6113914
; GENERAL INFORMATION:
; APPLICANT: SIMON, MARKUS
; APPLICANT: KRAMER, MICHAEL
; APPLICANT: SCHABBLE, ULRICH
```

```

; APPLICANT: WALLICH, REINHARD
; APPLICANT: LOBET, YVES
; TITLE OF INVENTION: OSP A PROTEINS OF BORRELIA BURGDORFERI SUBGROUPS, ENCODING GE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SMITHKLINE BEECHAM CORPORATION/CORPORATE INTELLECTUAL PROPERTY-UW
; STREET: P.O. BOX 1539
; CITY: KING OF PRUSSIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/193,159
; FILING DATE: JULY 5, 1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: JEFFREY A. SUTTON
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: B45008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270 5024
; TELEFAX: (610) 270 5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 337 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: BORRELIA BURGDORFERI
; STRAIN: 19857
; IMMEDIATE SOURCE:
; CLONE: NS1-19857
; US-08-193-159-8

```

```

Query Match 33.1%; Score 390.5; DB 2; Length 337;
Best Local Similarity 42.4%; Pred. No. 2.3e-35;
Matches 112; Conservative 21; Mismatches 58; Indels 73; Gaps 10;

QY 1 MDSNTVSSFQVDCFLMHWKRFADQELGDPFLDRLRRDQKSLKGRGSLGLDIETATRA 60
DB 1 MDPNTVSSFQVDSFLMHWKRVADQELGDPFLDRLRRDQKSLKGRGSLGLDIETATRA 60
QY 61 GKQIVQEILEESDEALKMTIASVPASRYLTDWTLDEMRS-----DWFMLMPKQKVTG 113
DB 61 GKQIVQEILEESDEALKMTGKQNV-----SLDEKNSVSDVPDGMKVLVSKENKD 114
QY 114 SLICRMDQAIMDKNIILKA-----NFSVIFERLE-----TLILRAFTREG 154
DB 115 G----KYDLMATVDNVDLKGTSKNGSGILEGVKADKSKVLTAVDDLKTTLEVLKEDG 171
QY 155 AVV-----TVRISE---TLOR 200
DB 172 TVSVKRVTSKDKSTTEAKFNKSGELSEKMTWTRANGTTTLEYSQMTNEDNAKAVETLKNGI 231
QY 186 KWNND-----TVRISE---TLOR 200
DB 232 KFEGLASGKTAVEIKEGTVTLKR 255

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RESULT 11
US-09-283-646C-8
; Sequence 8, Application US/09283646C
; Patent No. 6676942
; GENERAL INFORMATION:
; APPLICANT: Simon, Markus

```

```

; APPLICANT: Kramer, Michael
; APPLICANT: Schaible, Ulrich
; APPLICANT: Wallich, Reinhard
; APPLICANT: Lobet, Yves
; TITLE OF INVENTION: OSP A PROTEINS OF BORRELIA BURGDORFERI
; FILE REFERENCE: B45008-C1-C1
; CURRENT APPLICATION NUMBER: US/09/283,646C
; CURRENT FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 08/441,857
; PRIOR FILING DATE: 1995-05-16
; PRIOR APPLICATION NUMBER: 08/193,159
; PRIOR FILING DATE: 1994-07-05
; PRIOR APPLICATION NUMBER: PCT/EP92/01827
; PRIOR FILING DATE: 1992-08-11
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 337
; TYPE: PRT
; ORGANISM: BORRELIA BURGDORFERI
; US-09-283-646C-8

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Query Match 33.1%; Score 390.5; DB 2; Length 337;
Best Local Similarity 42.4%; Pred. No. 2.3e-35;
Matches 112; Conservative 21; Mismatches 58; Indels 73; Gaps 10;

QY 1 MDSNTVSSFQVDCFLMHWKRFADQELGDPFLDRLRRDQKSLKGRGSLGLDIETATRA 60
DB 1 MDPNTVSSFQVDSFLMHWKRVADQELGDPFLDRLRRDQKSLKGRGSLGLDIETATRA 60
QY 61 GKQIVQEILEESDEALKMTIASVPASRYLTDWTLDEMRS-----DWFMLMPKQKVTG 113
DB 61 GKQIVQEILEESDEALKMTGKQNV-----SLDEKNSVSDVPDGMKVLVSKENKD 114
QY 114 SLICRMDQAIMDKNIILKA-----NFSVIFERLE-----TLILRAFTREG 154
DB 115 G----KYDLMATVDNVDLKGTSKNGSGILEGVKADKSKVLTAVDDLKTTLEVLKEDG 171
QY 155 AVV-----TVRISE---TLOR 200
DB 172 TVSVKRVTSKDKSTTEAKFNKSGELSEKMTWTRANGTTTLEYSQMTNEDNAKAVETLKNGI 231
QY 186 KWNND-----TVRISE---TLOR 200
DB 232 KFEGLASGKTAVEIKEGTVTLKR 255

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RESULT 12
PCT-US94-01149-12
; Sequence 12, Application PC/TUS9401149
; GENERAL INFORMATION:
; APPLICANT: Shatzman, Allan
; APPLICANT: Scott, Miller
; APPLICANT: Dillon, Susan B.
; APPLICANT: Kane, James
; TITLE OF INVENTION: Vaccinal Polypeptides
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation - Corporate
; ADDRESS: Patents
; STREET: U.S. Mailcode UW2220 - 709 Swedeland Road
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01149

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;
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 149,150
; FILING DATE: 05-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 013,415
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 108,914
; FILING DATE: 18-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 837,773
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 751,896
; FILING DATE: 30-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 387,200
; FILING DATE: 28-JUL-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 238,801
; FILING DATE: 02-NOV-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 645,732
; FILING DATE: 30-AUG-1984
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P50134 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-270-5096
; TELEFAX: 215-270-5090
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-01149-12

Query Match 33.1%; Score 389.5; DB 4; Length 230;
Best Local Similarity 78.8%; Pred. No. 1.7e-35;
Matches 78; Conservative 8; Mismatches 10; Indels 3; Gaps 1;

Qy 1 MDSNTVSSFQVDCFLMHWKRPADQELGDAPFLDLRRDQKSLKRGSTGLGDIETATRA 60
Db 1 MDPNTVSSFQVDCFLMHWKRVADQELGDAPFLDLRRDQKSLKRGSTGLGDIETATRA 60
Qy 61 GKQIVEOILEESDEALKMTIASV---PASRYLTDMTLD 96
Db 61 GKQIVERILKEESDEALKMTMDHMLIQDLEKYVEDTKID 99

RESULT 13
PCT-US94-01149-72
; Sequence 72, Application PC/TUS9401149
; GENERAL INFORMATION:
; APPLICANT: Shatzman, Allan
; APPLICANT: Scott, Miller
; APPLICANT: Dillon, Susan B.
; APPLICANT: Kane, James
; TITLE OF INVENTION: Vaccinal Polypeptides
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation - Corporate
; ADDRESS: Patents
; STREET: U.S. Mailcode UW2220 - 709 Swedeland Road
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:

; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 149,150
; FILING DATE: 05-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 013,415
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 108,914
; FILING DATE: 18-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 837,773
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 751,896
; FILING DATE: 30-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 387,200
; FILING DATE: 28-JUL-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 238,801
; FILING DATE: 02-NOV-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 645,732
; FILING DATE: 30-AUG-1984
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P50134 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-270-5096
; TELEFAX: 215-270-5090
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-01149-72

Query Match 33.1%; Score 389.5; DB 4; Length 230;
Best Local Similarity 78.8%; Pred. No. 1.7e-35;
Matches 78; Conservative 8; Mismatches 10; Indels 3; Gaps 1;

Qy 1 MDSNTVSSFQVDCFLMHWKRPADQELGDAPFLDLRRDQKSLKRGSTGLGDIETATRA 60
Db 1 MDPNTVSSFQVDCFLMHWKRVADQELGDAPFLDLRRDQKSLKRGSTGLGDIETATRA 60
Qy 61 GKQIVEOILEESDEALKMTIASV---PASRYLTDMTLD 96
Db 61 GKQIVERILKEESDEALKMTMDHMLIQDLEKYVEDTKID 99

RESULT 14
PCT-US94-01149-55
; Sequence 55, Application PC/TUS9401149
; GENERAL INFORMATION:
; APPLICANT: Shatzman, Allan
; APPLICANT: Scott, Miller
; APPLICANT: Dillon, Susan B.
; APPLICANT: Kane, James
; TITLE OF INVENTION: Vaccinal Polypeptides
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation - Corporate
; ADDRESS: Patents
```

STREET: U.S. Mailcode UW2220 - 709 Swedeland Road
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01149
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 149,150
FILING DATE: 05-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 013,415
FILING DATE: 01-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 108,914
FILING DATE: 18-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 837,773
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 751,896
FILING DATE: 30-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 387,200
FILING DATE: 28-JUL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 238,801
FILING DATE: 02-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 645,732
FILING DATE: 30-AUG-1984
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50134 PCT
TELEPHONE: 215-270-5096
TELEFAX: 215-270-5090
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 304 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-01149-55

Query Match 33.1%; Score 389.5; DB 4; Length 304;
Best Local Similarity 37.9%; Pred. No. 2.5e-35;
Matches 99; Conservative 36; Mismatches 47; Indels 79; Gaps 7;
Qy 1 MDSNTVSSFOVDFLHVHVRKRFADQELGAPFLDLRRDQKSLKGRGSLGLDIETATRA 60
Db 1 MDPNTVSSFOVDFLHVHVRKRVADQELGAPFLDLRRDQKSLKGRGSLGLDIETATRA 60
Qy 61 GKQIVQEILLESDEALKMTI-----ASVPASRY 89
Db 61 GKQIVERILKEESDEALKMTMGFGAIFLEGCGWEGHGYTSHCAHGAVAADLK 120
Qy 90 LTDMTLDMSRDWMLMP-----KQKVTGSL-----CIRMDQAINDKNIIILKANESVIP 138
Db 121 STQEAINKITKNLYLSELVKNLQELSGANNELHDELDKVD-----LRAD--TIS 174
Qy 139 ERLEVLIIIRAFTEGAVGCEISPLSPFGHTNEDVKNALGVILGKKNQNTVRISETL 198
Db 175 SQELAVLL---SNEGINS-----DEHLALERKL 203

Qy 199 ORFAWRSSHENGRSPFPKQK 219
Db 204 KKMGLGPSAVEIGNGCFETKHK 224
RESULT 15
PCT-US94-01149-57
Sequence 57, Application PC/TUS9401149
GENERAL INFORMATION:
APPLICANT: Shatzman, Allan
APPLICANT: Scott, Miller
APPLICANT: Dillo, Susan B.
APPLICANT: Kane, James
TITLE OF INVENTION: Vaccinal Polypeptides
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation - Corporate
ADDRESSEE: Patents
STREET: U.S. Mailcode UW2220 - 709 Swedeland Road
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01149
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 149,150
FILING DATE: 05-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 013,415
FILING DATE: 01-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 108,914
FILING DATE: 18-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 837,773
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 751,896
FILING DATE: 30-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 387,200
FILING DATE: 28-JUL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 238,801
FILING DATE: 02-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 645,732
FILING DATE: 30-AUG-1984
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50134 PCT
TELEPHONE: 215-270-5096
TELEFAX: 215-270-5090
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 304 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-01149-57

Query Match 33.1%; Score 389.5; DB 4; Length 304;
Best Local Similarity 37.9%; Pred. No. 2.5e-35;

Matches		99; Conservative	36; Mismatches	47; Indels	79; Gaps	7;
Qy	1	MDSNTVSSFOVDCFLHVRKRPADQELGDAPFLDRLRRDOKSLKRGSTGLDIDTETATRA	60			
Db	1	MDPNTVSSFOVDCFLHVRKRVADQELGDAPFLDRLRRDOKSLRGRSTGLDIDTETATRA	60			
Qy	61	GKQIVEQIIEESDEALKMTI-----ASVPASRY	89			
Db	61	GKQIVERILKEESDEALKMTGFGAIAAGFLEGGWEGMIAGWHGYTSHGAHVAVAADLK	120			
Qy	90	LTDMTLDEMSRDWFMFLMP-----KQKVTGSL-----CIRMDQAIMDKNIIILKANFSVIF	138			
Db	121	STQEAINKITKNLNYLSELEVKNLQRLSGAMNELHDEILEDEKVDD-----LRAD--TIS	174			
Qy	139	ERLETLLIRAFTEEGAVVGEISPLSPFGHTNEDVKNAIGVLIGLKNWNTVRISETL	198			
Db	175	SOIELAVLL---SNEGIINSE-----DEHLALERKL	203			
Qy	199	QRFWRSSHENGSRPSPPKOK	219			
Db	204	KKMLGFSAVEIGNGCFETKHK	224			

Search completed: March 7, 2006, 19:22:42
Job time : 49 secs

GenCore version S.1.7
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OM protein - protein search, using sw model

Run on: March 7, 2006, 19:17:24 ; Search time 40 Seconds
(without alignments)
553.246 Million cell updates/sec

Title: US-10-734-373-58
Perfect score: 1178
Sequence: 1 MDSNTVSSFQVDCFLWHVRK.....RPSFPKQKRMERTIEPV 230

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query #	Score	Match	Length	DB	ID	Description
1	1	1110	94.2	230	1	MNIVA2	nonstructural prot
2	2	1097	93.1	230	1	MNIVA3	nonstructural prot
3	3	1083	92.8	230	1	MNIVA4	nonstructural prot
4	4	1083	91.9	227	1	MNIVX9	nonstructural prot
5	5	1075	91.3	230	1	MNIV1F	nonstructural prot
6	6	1074	91.2	227	1	MNIVX3	nonstructural prot
7	7	1073	91.1	230	1	MNIVA1	nonstructural prot
8	8	1066	90.5	227	1	MNIVC5	nonstructural prot
9	9	1055	89.6	237	1	MNIVX1	nonstructural prot
10	10	1054	89.5	227	1	MNIV77	nonstructural prot
11	11	1054	89.5	237	1	MNIV14	nonstructural prot
12	12	1053	89.4	237	1	MNIV77	nonstructural prot
13	13	1052	89.3	230	1	MNIV1	nonstructural prot
14	14	1051	89.2	227	1	MNIVX1	nonstructural prot
15	15	1048	89.0	230	2	S09648	nonstructural prot
16	16	1041	88.4	230	1	D45539	nonstructural prot
17	17	1010	85.7	237	1	MNIVA1	nonstructural prot
18	18	1007	85.5	237	1	MNIV61	nonstructural prot
19	19	995	84.5	217	1	MNIV1K	nonstructural prot
20	20	949	80.6	202	1	MNIV47	nonstructural prot
21	21	852	72.3	230	1	MNIV16	nonstructural prot
22	22	848	72.0	230	1	MNIVA5	nonstructural prot
23	23	848	72.0	230	1	MNIVA6	nonstructural prot
24	24	846	71.8	230	1	MNIVA8	nonstructural prot
25	25	845	71.7	230	2	MNIVA7	nonstructural prot
26	26	833	70.7	230	2	A45575	nonstructural prot
27	27	429	36.4	124	1	MNIV71	nonstructural prot
28	28	406	34.5	89	2	B92982	nonstructural prot
29	29	149	12.6	32	2	PQ0419	nonstructural prot

ALIGNMENTS

RESULT 1
MNTVA2

nonstructural protein NS1 - influenza A virus (strain A/mallard/New York/6750/78)
 C:Species: Influenza A virus
 C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
 C:Accession: C32662
 R:Treanor, J. J.; Snyder, M. H.; London, W. T.; Murphy, B. R.
 J Virol 171, 1-9, 1999
 A:Title: The B allele of the NS gene of avian influenza viruses, but not the A al
 A:Reference number: A32662; MUID:89299445; PMID:2525836
 A:Accession: C32662
 A:Molecule type: genomic RNA
 A:Residues: 1-230 <TRE>
 A:Cross-references: UNIPROT:P13138; UNIPARC:UPI0000174ABA

Query Match	94.2%;	Score 1110;	DB 1;	Length 230;
Best Local Similarity	93.5%;	Pred. No. 3.2e-87;		
Matches 215;	Conservative 9;	Mismatches 6;	Indels 0;	Gaps 0
QY	1	MSDSNTVSSFOVDCFLMHVKRKFADQELGAPDFDLRLRRDQSKLGRGSLGLDIETATRA	60	
Db	1	MSDSNTVSSFOVDCFLMHVKRKFADQELGAPDFDLRLRRDQSLRGRGSLGLDIETATRA	60	
QY	61	GKQIVETQLBEEDEALQMTIASVPASRYLTQMTLDENSRDWPMLPQKQVTGSLCIRMD	120	
Db	61	GKQIVETQLBEEDEALQMTIASVPASRYLTQMTLEENSRDWPMLPQKQVAGSLCIRMD	120	
QY	121	QAIMDKNTILKANFSPVIFERLETILLRAFTTEGAVGEISPLSPISPGHNTVEDVKNAIGV	180	
Db	121	QAIMDKNTILKANFSPVIFERLETILLRAFTTEGAVGEISPLSPISPGHNTVEDVKNAIGV	180	
QY	181	LIGGLKMNNDNTVAISSETLQRFAMWSSHENGRRSPFPQKQKMMERTITEPEV	230	
Db	181	LIGGLEWNDNTVAISSETLQRFAMWSSHENGRRPPLPQKQKMMERTITEPEV	230	

RESULT 2

MN13A3
 nonstructural protein NS1 - influenza A virus (strain A/mallard/New York/6874/78)
 C-Species: Influenza A virus
 C-Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 08-Jul-2004
 C-Accession: E33662
 R-IsFrom: J.J.; Snyder, M.H.; London, W.T.; Murphy, B.R.
 R-Virology 171, 1-9, 1989
 A-Title: The B allele of the NS gene of avian influenza viruses, but not the A al
 A-Reference number: A32662; MUID:89299445; PMID:2525836
 A-Accession: E33662

nonstructural protein NS1 - influenza A virus (strain A/Mynah/Haneda-Thai/76 [H3N1]) (fr.
C:Species: influenza A virus
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C:Accession: U0000174ABE
R:Nakajima, K.; Nobusawa, E.; Ogawa, T.; Nakajima, S.
Virology 158, 465-468, 1987
A:Title: Genetic divergence of the NS genes of avian influenza viruses.
A:Reference number: A94361; MUID:87236215; PMID:2954302
A:Accession: 127846
A:Molecule type: genomic RNA
A:Residues: 1-227 <NA>
A:Cross-references: UNIPARC:UPI0000138A5C; GB:M17070; NID:G324854; PIDN:AAA43548.1; PID:
C:Genetics: NS1
A:Map position: segment 8
C:Superfamily: influenza virus nonstructural protein NS1
C:Keywords: alternative splicing; nonstructural protein

Query Match 93.1%; Score 1097; DB 1; Length 230;
Best Local Similarity 92.6%; Pred. No. 4.1e-86; Indels 0; Gaps 0;
Matches 213; Conservative 9; Mismatches 8

QY 1 MDSNTVSSFQVDCFLMHWKRFADQELGDAPFLDLRRDQSKLGRGSLGLDLETATRA 60
DB 1 MDSNTVSSFQVDCFLMHWKRFADQELGDAPFLDLRRDQSKLGRGSLGLDLETATRA 60
QY 61 GKQIVQEILLESDEALKMTIASVPASRYLTDMLDEMSRDWFMMPKQKVTGSLCIRMD 120
DB 61 GKQIVQEILLESDEALKMTIASVPASRYLTDMLDEMSRDWFMMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTTEGAVGEISPLPSLPKGTNEDVKNAGV 180
DB 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTTEGAVGEISPLPSLPKGTNEDVKNAGV 180
QY 181 LIGGLKWNNTVRISETLQRFAMRSSHENGSRPFPKQKRWERTIEPEV 230
DB 181 LIGGLEWNTVRSVETLQRFAMRSSHENGSRPFPKQKRWERTIEPEV 230

RESULT 3
MNIV4
nonstructural protein NS1 - influenza A virus (strain A/pintail/Alberta/119/79)
C:Species: influenza A virus
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: G32662
R:Frenco, J. J.; Snyder, M.H.; London, W.T.; Murphy, B.R.
Virology 171, 1-9, 1989
A:Title: The B allele of the NS gene of avian influenza viruses, but not the A allele,
A:Reference number: A32662; MUID:89299445; PMID:2525836
A:Accession: G32662
A:Molecule type: genomic RNA
A:Residues: 1-230 <TRE>
A:Cross-references: UNIPROT:P13140; UNIPARC:UPI0000174ABC
C:Genetics: NS1
A:Map position: segment 8
C:Superfamily: influenza virus nonstructural protein NS1
C:Keywords: alternative splicing; nonstructural protein

Query Match 92.8%; Score 1093; DB 1; Length 230;
Best Local Similarity 92.2%; Pred. No. 9e-86; Indels 0; Gaps 0;
Matches 212; Conservative 9; Mismatches 9

QY 1 MDSNTVSSFQVDCFLMHWKRFADQELGDAPFLDLRRDQSKLGRGSLGLDLETATRA 60
DB 1 MDSNTVSSFQVDCFLMHWKRFADQELGDAPFLDLRRDQSKLGRGSLGLDLETATRA 60
QY 61 GKQIVQEILLESDEALKMTIASVPASRYLTDMLDEMSRDWFMMPKQKVTGSLCIRMD 120
DB 61 GKQIVQEILLESDEALKMTIASVPASRYLTDMLDEMSRDWFMMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTTEGAVGEISPLPSLPKGTNEDVKNAGV 180
DB 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTTEGAVGEISPLPSLPKGTNEDVKNAGV 180
QY 181 LIGGLKWNNTVRISETLQRFAMRSSHENGSRPFPKQKRWERTIEPEV 230
DB 181 LIGGLEWNTVRSVETLQRFAMRSSHENGSRPFPKQKRWERTIEPEV 230

RESULT 4
MNIVX9

nonstructural protein NS1 - influenza A virus (strain A/Mynah/Haneda-Thai/76 [H3N1]) (fr.
C:Species: influenza A virus
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C:Accession: 127846
R:Nakajima, K.; Nobusawa, E.; Ogawa, T.; Nakajima, S.
Virology 158, 465-468, 1987
A:Title: Genetic divergence of the NS genes of avian influenza viruses.
A:Reference number: A94361; MUID:87236215; PMID:2954302
A:Accession: 127846
A:Molecule type: genomic RNA
A:Residues: 1-227 <NA>
A:Cross-references: UNIPARC:UPI0000138A5C; GB:M17070; NID:G324854; PIDN:AAA43548.1; PID:
C:Genetics: NS1
A:Map position: segment 8
C:Superfamily: influenza virus nonstructural protein NS1
C:Keywords: alternative splicing; nonstructural protein

Query Match 93.1%; Score 1097; DB 1; Length 230;
Best Local Similarity 92.6%; Pred. No. 4.1e-86; Indels 0; Gaps 0;
Matches 213; Conservative 9; Mismatches 8

QY 1 MDSNTVSSFQVDCFLMHWKRFADQELGDAPFLDLRRDQSKLGRGSLGLDLETATRA 60
DB 1 MDSNTVSSFQVDCFLMHWKRFADQELGDAPFLDLRRDQSKLGRGSLGLDLETATRA 60
QY 61 GKQIVQEILLESDEALKMTIASVPASRYLTDMLDEMSRDWFMMPKQKVTGSLCIRMD 120
DB 61 GKQIVQEILLESDEALKMTIASVPASRYLTDMLDEMSRDWFMMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTTEGAVGEISPLPSLPKGTNEDVKNAGV 180
DB 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTTEGAVGEISPLPSLPKGTNEDVKNAGV 180
QY 181 LIGGLKWNNTVRISETLQRFAMRSSHENGSRPFPKQKRWERTIEPEV 230
DB 181 LIGGLEWNTVRSVETLQRFAMRSSHENGSRPFPKQKRWERTIEPEV 230

RESULT 3
MNIV4
nonstructural protein NS1 - influenza A virus (strain A/pintail/Alberta/119/79)
C:Species: influenza A virus
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: G32662
R:Frenco, J. J.; Snyder, M.H.; London, W.T.; Murphy, B.R.
Virology 171, 1-9, 1989
A:Title: The B allele of the NS gene of avian influenza viruses, but not the A allele,
A:Reference number: A32662; MUID:89299445; PMID:2525836
A:Accession: G32662
A:Molecule type: genomic RNA
A:Residues: 1-230 <TRE>
A:Cross-references: UNIPROT:P13140; UNIPARC:UPI0000174ABC
C:Genetics: NS1
A:Map position: segment 8
C:Superfamily: influenza virus nonstructural protein NS1
C:Keywords: alternative splicing; nonstructural protein

Query Match 92.8%; Score 1093; DB 1; Length 230;
Best Local Similarity 92.2%; Pred. No. 9e-86; Indels 0; Gaps 0;
Matches 212; Conservative 9; Mismatches 9

QY 1 MDSNTVSSFQVDCFLMHWKRFADQELGDAPFLDLRRDQSKLGRGSLGLDLETATRA 60
DB 1 MDSNTVSSFQVDCFLMHWKRFADQELGDAPFLDLRRDQSKLGRGSLGLDLETATRA 60
QY 61 GKQIVQEILLESDEALKMTIASVPASRYLTDMLDEMSRDWFMMPKQKVTGSLCIRMD 120
DB 61 GKQIVQEILLESDEALKMTIASVPASRYLTDMLDEMSRDWFMMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTTEGAVGEISPLPSLPKGTNEDVKNAGV 180
DB 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTTEGAVGEISPLPSLPKGTNEDVKNAGV 180
QY 181 LIGGLKWNNTVRISETLQRFAMRSSHENGSRPFPKQKRWERTIEPEV 230
DB 181 LIGGLEWNTVRSVETLQRFAMRSSHENGSRPFPKQKRWERTIEPEV 230

RESULT 4
MNIVX9

nonstructural protein NS1 - influenza A virus
C:Species: influenza A virus
C:Date: 31-Oct-1980 #sequence_revision 31-Oct-1980 #text_change 30-Sep-1993
C:Accession: A04091
R:Porter, A.G.; Smith, J.C.; Emtage, J.S.
Proc. Natl. Acad. Sci. U.S.A. 77, 5074-5078, 1980
A:Title: Nucleotide sequence of influenza virus RNA segment 8 indicates that coding regi
A:Reference number: A93858; MUID:81054909; PMID:6254054
A:Accession: A04091
A:Molecule type: mRNA
A:Residues: 1-230 <POR>
A:Cross-references: UNIPARC:UPI0000138A58
A:Experimental source: strain Rostock
C:Superfamily: influenza virus nonstructural protein NS1
C:Keywords: alternative splicing

Query Match 91.3%; Score 1075; DB 1; Length 230;
Best Local Similarity 89.1%; Pred. No. 3.1e-84; Indels 0; Gaps 0;
Matches 205; Conservative 16; Mismatches 9

QY 1 MDSNTVSSFQVDCFLMHWKRFADQELGDAPFLDLRRDQSKLGRGSLGLDLETATRA 60
DB 1 MDSNTVSSFQVDCFLMHWKRFADQELGDAPFLDLRRDQSKLGRGSLGLDLETATRA 60
QY 61 GKQIVQEILLESDEALKMTIASVPASRYLTDMLDEMSRDWFMMPKQKVTGSLCIRMD 120
DB 61 GKQIVQEILLESDEALKMTIASVPASRYLTDMLDEMSRDWFMMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTTEGAVGEISPLPSLPKGTNEDVKNAGV 180
DB 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTTEGAVGEISPLPSLPKGTNEDVKNAGV 180

C;Keywords: alternative splicing; nonstructural protein

Query Match 89.6%; Score 1055; DB 1; Length 237;
Best Local Similarity 88.3%; Pred. No. 1.6e-82;
Matches 203; Conservative 13; Mismatches 14; Indels 0; Gaps 0;
QY 1 MDSNTVSSFOVDCFLMHVVRKPADQELGDAPFLDRLRRDQKSLKGRGSLGLDIETATRA 60
DB 1 MDNTVSSFOVDCFLMHVVRKQVADQELGDAPFLDRLRRDQKSLKGRGSLGLDIETATCV 60
QY 61 GKQIVQILLESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMD 120
DB 61 GKQIVVERILKEESDEALKMTMASAPASRYLTDMTIEMSRDWMFMPKQKVGAPLCVRMD 120
QY 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTTEGAVGEISPLSPGHTNEDVKNAIGV 180
DB 121 QAIMDKNIIILKANFSVIFDRLETLILLRAFTTEGAVGEISPLSPGHTNEDVKNAIGV 180
QY 181 LIGGLKNDNTVRISSETLORFAWRSHENGSRPFPKQKRMERTIEPEV 230
DB 181 LIGGLEWNTVVRVSKTLORFAWRSSNENGRPPLTPKQKRMARIRSEV 230

RESULT 10

MNIVX7
nonstructural protein NS1 - influenza A virus (strain A/Duck/Ukraine/63 [H3N8]) (fragment)
C;Species: influenza A virus
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C;Accession: G27846
R;Nakajima, K.; Nobusawa, E.; Ogawa, T.; Nakajima, S.
Virology 158, 465-468, 1987
A;Title: Genetic divergence of the NS genes of avian influenza viruses.
A;Reference number: A94361; MUID:87236215; PMID:2954302

A;Accession: G27846

A;Molecule type: genomic RNA

A;Residues: 1-227 <NA>

A;Cross-references: UNIPARC:UPI0000138A55; GB:M16565; NID:G324789; PIDN:AAA43512.1; PID:

C;Genetics:

A;Map position: segment 8

C;Superfamily: influenza virus nonstructural protein NS1

C;Keywords: alternative splicing; nonstructural protein

Query Match 89.5%; Score 1054; DB 1; Length 227;
Best Local Similarity 89.9%; Pred. No. 1.9e-82;
Matches 204; Conservative 12; Mismatches 11; Indels 0; Gaps 0;
QY 4 NTVSSFOVDCFLMHVVRKPADQELGDAPFLDRLRRDQKSLKGRGSLGLDIETATRAKQ 63
DB 1 NTVSSFOVDCFLMHVVRKPADQELGDAPFLDRLRRDQKSLKGRGSLGLDIETATRAKQ 60
QY 64 IVEQILLESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMDQAI 123
DB 61 TVERILLESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMDQAI 120
QY 124 MDKNIIILKANFSVIFERLETLILLRAFTTEGAVGEISPLSPGHTNEDVKNAIGV 183
DB 121 MDKDIILKANFSVIFERLETLILLRAFTTEGAVGEISPLSPGHTNEDVKNAIGV 180
QY 184 GLKNDNTVRISSETLORFAWRSHENGSRPFPKQKRMERTIEPEV 230
DB 181 GLEWNTVVRVSKTLORFAWRSSNENGRPPLTPKQKRMARIRSEV 227

RESULT 11

MNIV14
nonstructural protein NS1 - influenza A virus (strain A/FW/1/50 [H1N1])
C;Species: influenza A virus
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 16-Jul-1999
C;Accession: A92991; A04090; B92982
R;Krystal, M.; Buonagurio, D.; Young, J.F.; Palese, P.
J. Virol. 45, 547-554, 1983
A;Title: Sequential mutations in the NS genes of influenza virus field strains.

A;Reference number: A92991; MUID:83164298; PMID:6834468

A;Accession: A92991

A;Molecule type: Genomic RNA

A;Residues: 1-237 <XRY>

A;Cross-references: UNIPARC:UPI0000138A57; GB:K00576; NID:G324813; PIDN:AAA43525.1; PID:

C;Genetics:

A;Map position: segment 8

C;Superfamily: influenza virus nonstructural protein NS1

C;Keywords: alternative splicing

Query Match 89.5%; Score 1054; DB 1; Length 237;
Best Local Similarity 88.3%; Pred. No. 2e-82;
Matches 203; Conservative 14; Mismatches 13; Indels 0; Gaps 0;
QY 1 MDSNTVSSFOVDCFLMHVVRKPADQELGDAPFLDRLRRDQKSLKGRGSLGLDIETATRA 60
DB 1 MDNTVSSFOVDCFLMHVVRKQVADQELGDAPFLDRLRRDQKSLKGRGSLGLDIETATRV 60
QY 61 GKQIVQILLESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMD 120
DB 61 GKQIVVERILKEESDEALKMTMASAPASRYLTDMTIEMSRDWMFMPKQKVGAPLCIRMD 120
QY 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTTEGAVGEISPLSPGHTNEDVKNAIGV 180
DB 121 QAIMDKNIIILKANFSVIFDRLETLILLRAFTTEGAVGEISPLSPGHTNEDVKNAIGV 180
QY 181 LIGGLKNDNTVRISSETLORFAWRSHENGSRPFPKQKRMERTIEPEV 230
DB 181 LIGGLEWNTVVRVSKTLORFAWRSSNENGRPPLTPKQKRMARIRSEV 230

RESULT 12

MNIV77
nonstructural protein NS1 - influenza A virus (strain A/USSR/90/77 [H1N1])
C;Species: influenza A virus
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 16-Jul-1999
C;Accession: E92991; A04090
R;Krystal, M.; Buonagurio, D.; Young, J.F.; Palese, P.
J. Virol. 45, 547-554, 1983
A;Title: Sequential mutations in the NS genes of influenza virus field strains.
A;Reference number: A92991; MUID:83164298; PMID:6834468
A;Accession: E92991
A;Molecule type: genomic RNA
A;Residues: 1-237 <XRY>

A;Cross-references: UNIPARC:UPI0000138A66; GB:K00578; NID:G324839; PIDN:AAA43540.1; PID:

C;Genetics:

A;Map position: segment 8

C;Superfamily: influenza virus nonstructural protein NS1

C;Keywords: alternative splicing

Query Match 89.4%; Score 1053; DB 1; Length 237;
Best Local Similarity 88.3%; Pred. No. 2.4e-82;
Matches 203; Conservative 14; Mismatches 13; Indels 0; Gaps 0;
QY 1 MDSNTVSSFOVDCFLMHVVRKPADQELGDAPFLDRLRRDQKSLKGRGSLGLDIETATRA 60
DB 1 MDNTVSSFOVDCFLMHVVRKQVADQELGDAPFLDRLRRDQKSLKGRGSLGLDIETATCV 60
QY 61 GKQIVQILLESDEALKMTIASVPASRYLTDMLDMSRDWFMMPKQKVTGSLCIRMD 120
DB 61 GKQIVVERILKEESDEALKMTMASAPASRYLTDMTIEMSRDWMFMPKQKVGAPLCIRMD 120
QY 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTTEGAVGEISPLSPGHTNEDVKNAIGV 180
DB 121 QAIMDKNIIILKANFSVIFDRLETLILLRAFTTEGAVGEISPLSPGHTNEDVKNAIGV 180
QY 181 LIGGLKNDNTVRISSETLORFAWRSHENGSRPFPKQKRMERTIEPEV 230
DB 181 LIGGLEWNTVVRVSKTLORFAWRSSNENGRPPLTPKQKRMARIRSEV 230

RESULT 13

MNIV1

nonstructural protein NS1 - influenza A virus (strain A/PR/8/34)
C:Species: influenza A virus
C:Date: 30-Apr-1981 #sequence_revision 30-Apr-1981 #text_change 30-Sep-1993
C:Accession: A04089
R:Baes, M.; Taussig, R.; Zazza, J.J.; Young, J.F.; Palese, P.; Reisfeld, A.; Skalka, A.M.
Nucleic Acids Res. 8, 5845-5858, 1980
A:Title: Complete nucleotide sequence of the influenza A/PR/8/34 virus NS gene and comparison with other influenza A virus NS genes
A:Reference number: A93714; MUID:81124304; PMID:7465426
A:Accession: A04089
A:Molecule type: genomic RNA
A:Residues: 1-230 <BAE>
A:Cross-references: UNIPARC:UPI00000016F6
C:Genetics:
A:Map position: segment 8
C:Superfamily: influenza virus nonstructural protein NS1
C:Keywords: alternative splicing

Query Match 89.3%; Score 1052; DB 1; Length 230;
Best Local Similarity 88.7%; Pred. No. 2.8e-82;
Matches 204; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 MDSNTVSSFOVDCFLMHWKRFADQELGDAPFLDRLRRDQSLKGRGSLGLDIETATRA 60
DB 1 MDPNTVSSFOVDCFLMHWKRFADQELGDAPFLDRLRRDQSLKGRGSLGLDIETATRA 60
QY 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMTLEMSRDWFMMPKQKVTGSLCIRMD 120
DB 61 GKQIVERILKEESDEALKMTIASVPASRYLTDMTLEMSRDWFMMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTTEGAVGVEISPLSLPGHTNEDVKNAGV 180
DB 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTTEGAVGVEISPLSLPGHTNEDVKNAGV 180
QY 181 LIGGLKWNNTVRISETLQRFARSSHENGRPSFPKQKRMERTIEPEV 230
DB 181 LIGGLEWNTVVRVSETLQRFARSSNENGRPPLTPKQKREMGATIRSEV 230

RESULT 14

nonstructural protein NS1 - influenza A virus (strain A/Chicken/Japan/24 [H7N7]) (fragment)
C:Species: influenza A virus
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C:Accession: A27846
R:Nakajima, K.; Nobusawa, E.; Ogawa, T.; Nakajima, S.
Virology 159, 465-468, 1987
A:Title: Genetic divergence of the NS genes of avian influenza viruses.
A:Reference number: A94361; MUID:87236215; PMID:2954302
A:Accession: A27846
A:Molecule type: genomic RNA
A:Residues: 1-227 <NAK>
A:Cross-references: UNIPARC:UPI0000138A52; GB:M16561; NID:g324777; PIDN:AAA43504.1; PID:
C:Genetics:
A:Gene: NS1
A:Map position: segment 8
C:Superfamily: influenza virus nonstructural protein NS1
C:Keywords: alternative splicing; nonstructural protein

Query Match 89.2%; Score 1051; DB 1; Length 227;
Best Local Similarity 90.3%; Pred. No. 3.4e-82;
Matches 205; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 4 NTVSSFOVDCFLMHWKRFADQELGDAPFLDRLRRDQSLKGRGSLGLDIETATRA 63
DB 1 NTVSSFOVDCFLMHWKRFADQELGDAPFLDRLRRDQSLKGRGSLGLDIETATRA 60
QY 64 IVEQILEESDEALKMTIASVPASRYLTDMTLEMSRDWFMMPKQKVTGSLCIRMDQAI 123
DB 61 IVERILEESDETLKMTIASAPAPRYPTDMLTEMSRDWFMMPKQKVTGSLCIRMDQAI 120
QY 124 MDKNIIILKANFSVIFERLETLILLRAFTTEGAVGVEISPLSLPGHTNEDVKNAGV 183
DB 121 MDKNIIILKANFSVIFERLETLILLRAFTTEGAVGVEISPLSLPGHTNEDVKNAGV 180

QY 184 GLKWNNTVRISETLQRFARSSHENGRPSFPKQKRMERTIEPEV 230
DB 181 GLEWNTVVRVSETLQRFARSSNENGRPPLTPKQKREMGATIRSEV 230
RESULT 15
nonstructural protein NS1 - influenza A virus (strain A/Leningrad/1/54)
C:Species: influenza A virus
C:Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 19-May-2000
C:Accession: S09648
R:Beklemishev, A.B.; Blinov, V.M.; Vassilenko, S.K.; Golovin, S.Y.; Karginov, V.A.; Mana
Bicoglu, Khim. 11, 641-645, 1985
A:Title: Synthesis, cloning and sequencing of a full-length DNA copy of the fragment 8 c
A:Reference number: S09648; MUID:85307107; PMID:4038350
A:Accession: S09648
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-230 <BEK>
A:Cross-references: UNIPARC:UPI0000000533; EMBL:X52146; NID:g60716; PIDN:CAA36392.1; PID:
C:Superfamily: influenza virus nonstructural protein NS1

Query Match 89.0%; Score 1048; DB 2; Length 230;
Best Local Similarity 88.3%; Pred. No. 6.2e-82;
Matches 203; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 1 MDSNTVSSFOVDCFLMHWKRFADQELGDAPFLDRLRRDQSLKGRGSLGLDIETATRA 60
DB 1 MDPNTVSSFOVDCFLMHWKRFADQELGDAPFLDRLRRDQSLKGRGSLGLDIETATRA 60
QY 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMTLEMSRDWFMMPKQKVTGSLCIRMD 120
DB 61 GKQIVERILKEESDEALKMTIASVPASRYLTDMTLEMSRDWFMMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTTEGAVGVEISPLSLPGHTNEDVKNAGV 180
DB 121 QAIMDKNIIILKANFSVIFERLETLILLRAFTTEGAVGVEISPLSLPGHTNEDVKNAGV 180
QY 181 LIGGLKWNNTVRISETLQRFARSSHENGRPSFPKQKRMERTIEPEV 230
DB 181 LIGGLEWNTVVRVSETLQRFARSSNENGRPPLTPKQKREMGATIRSEV 230

Search completed: March 7, 2006, 19:21:49
Job time : 41 secs

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OM protein - protein search, using sw model

Run on: March 7, 2006, 19:13:44 ; Search time 186 Seconds
(without alignments)
543.318 Million cell updates/sec

Title: US-10-734-373-58
Perfect score: 1178
Sequence: 1 MDSNTVSSQVDCFLWVRK.....RPSFPKOKRMERTIEPV 230

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1178	100.0	230	4	Aae09027 Equine in
2	1178	100.0	230	4	Aae09029 Equine in
3	1165	98.9	230	2	Aaw03522 Non-struct
4	1099	93.3	230	8	Ado14175 Influenza
5	1083	91.9	227	8	Ado14179 Influenza
6	1066	90.5	227	8	Ado14177 Influenza
7	1066	90.5	230	8	Ado14174 Influenza
8	1061	90.1	238	9	Ady62119 Influenza
9	1059	89.9	230	8	Ado14183 Influenza
10	1055	89.6	237	5	Aae23116 Influenza
11	1052	89.3	230	9	Ady62121 Mutant in
12	1051	89.2	227	8	Ado14180 Influenza
13	1048	89.0	230	8	Ado14171 Influenza
14	1042	88.5	230	8	Ado14176 Influenza
15	1017	85.7	237	5	Abb05772 Influenza
16	1007	85.5	217	8	Ado14178 Influenza
17	953	80.9	202	8	Ado14184 Influenza
18	856	72.7	230	8	Ado14172 Influenza
19	852	72.3	230	8	Ado14181 Influenza
20	789	67.0	173	8	Ado14173 Influenza
21	586	49.7	193	9	Ady90024 Caspase c
22	488	41.4	197	4	Aae09028 Equine in
23	429	36.4	124	8	Ado14182 Influenza
24	400.5	34.0	246	2	Aaw12714 Flu NS1-H

ALIGNMENTS

RESULT 1

Aae09027
ID AAE09027 standard; protein; 230 AA.

XX	AAE09027;				
XX	15-NOV-2001 (first entry)				
XX	Equine influenza virus H3N8 PeiwtlNS230 protein.				
XX	Equine influenza virus; ei; cold adaptation; temperature sensitivity;				
KW	vaccine; neiwtlNS891 DNA; PeiwtlNS230 protein.				
XX	Equine influenza virus H3N8.				
XX	WO200160849-A2.				
PD	23-AUG-2001.				
PF	16-FEB-2001; 2001WO-US005048.				
XX	16-FEB-2000; 2000US-00506286.				
XX	(UYPI-) UNIV PITTSBURGH.				
PA	Dwelling PW, Youngner JS;				
PI	WPI; 2001-522584/57.				
DR	N-PSDB; AADI5678.				
XX	Novel isolated equine influenza virus (wild-type and cold-adapted)				
PT	proteins and viruses containing nucleic acid molecules encoding the				
PT	proteins, which are useful for protecting animals from influenza virus				
PT	infections.				
XX	Claim 5; Page 72-73; 172pp; English.				
XX	The patent discloses cold-adapted equine influenza viruses and				
CC	reassortant influenza A viruses comprising at least one genome segment of				
CC	such an equine influenza virus, wherein the equine of the cold-adapted				
CC	segment confers at least one identifying phenotype of the cold-adapted				
CC	equine influenza virus, such as cold adaptation, temperature sensitivity,				
CC	dominant interference or attenuation. The viruses are useful for				
CC	protecting animals from diseases caused by influenza viruses. They are				
CC	also used as vaccines. The present sequence is an equine influenza (ei)				
CC	virus H3N8 Peiwtl (wild type) NS230 protein which is encoded by				
CC	neiwtlNS891 DNA				

25	400	34.0	344	4	ABU71886	Abu71886 Human pro
26	395	33.5	231	2	AAR20301	Aar20301 Val(1) to
27	392.5	33.3	306	2	AAR38867	Aar38867 Sequence
28	392.5	33.3	306	2	AAR60194	Aar60194 Immunogen
29	390.5	33.1	337	2	AAR33448	Aar33448 NS1-19857
30	389.5	33.1	230	2	AAR38868	Aar38868 Sequence
31	389.5	33.1	230	2	AAR60195	Aar60195 Immunogen
32	389.5	33.1	230	2	AAR60226	Aar60226 Immunogen
33	389.5	33.1	304	2	AAR60197	Aar60197 Immunogen
34	389.5	33.1	304	2	AAR60207	Aar60207 Immunogen
35	388	32.9	309	2	AAR13175	Aar13175 NS1_81-RL
36	388	32.9	319	2	AAR07945	Aar07945 NS181RLFA
37	388	32.9	319	2	AAR13176	Aar13176 NS1_81-RL
38	388	32.9	327	2	AAR13177	Aar13177 NS1_81-RL
39	387.5	32.9	225	2	AAR38879	Aar38879 Sequence
40	387.5	32.9	231	2	AAR60217	Aar60217 Immunogen
41	387.5	32.9	231	2	AAR38878	Aar38878 Sequence
42	387.5	32.9	242	2	AAR60216	Aar60216 D protein
43	387.5	32.9	242	2	AAR04208	Aar04208 D protein
44	387.5	32.9	242	2	AAR60209	Aar60209 Immunogen
45	387	32.9	312	4	AAY72521	Aay72521 NS1-P703P

XX Sequence 230 AA;
 Query Match 100.0%; Score 1178; DB 4; Length 230;
 Best Local Similarity 100.0%; Pred. No. 9.3e-118;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDSNTVSSFOVDCFLWHVRRKRFADQELGDAFLDLRLRRDQKSLKGRGSLGLDLETATRA 60
 DB 1 MDSNTVSSFOVDCFLWHVRRKRFADQELGDAFLDLRLRRDQKSLKGRGSLGLDLETATRA 60
 QY 61 GKQIVQIILEESDEALKNVTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
 DB 61 GKQIVQIILEESDEALKNVTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
 QY 121 QAIMDKNIIILKANFSVIFERLETLILRAFTTEGAVGEISPLPSLPGHTNEDVKNAIGV 180
 DB 121 QAIMDKNIIILKANFSVIFERLETLILRAFTTEGAVGEISPLPSLPGHTNEDVKNAIGV 180
 QY 181 LIGLKWNDNTVRISETLQRFARSSSHENGSRPSFPKQKRWERTIEPEV 230
 DB 181 LIGLKWNDNTVRISETLQRFARSSSHENGSRPSFPKQKRWERTIEPEV 230

RESULT 2
 AAE09029
 ID AAE09029 standard; protein; 230 AA.
 XX
 AC AAE09029;
 XX
 DT 15-NOV-2001 (first entry)
 XX
 DE Equine influenza virus H3N8 PeicalNS230 protein.
 XX
 KW Equine influenza virus; ei; cold adaptation; temperature sensitivity;
 KW vaccine; neicalNS988 DNA; PeicalNS230 protein.
 XX
 OS Equine influenza virus H3N8.
 XX
 PN WO200160849-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 16-FEB-2001; 2001WO-US005048.
 XX
 PR 16-FEB-2000; 2000US-00506286.
 XX
 PA (UYP1-) UNIV PITTSBURGH.
 XX
 PI Dowling PW, Youngner JS;
 XX
 DR WPI: 2001-522584/57.
 XX
 DR N-PSDB; AAD15681.

XX Novel isolated equine influenza virus (wild-type and cold-adapted)
 PT proteins and viruses containing nucleic acid molecules encoding the
 PT proteins, which are useful for protecting animals from influenza virus
 PT infections.
 XX
 PS Claim 5; Page 77; 172pp; English.
 XX
 CC The patent discloses cold-adapted equine influenza viruses and
 CC reassortant influenza A viruses comprising at least one genome segment of
 CC such an equine influenza virus, wherein the equine influenza virus genome
 CC segment confers at least one identifying phenotype of the cold-adapted
 CC equine influenza virus, such as cold adaptation, temperature sensitivity,
 CC dominant interference or attenuation. The viruses are useful for
 CC protecting animals from diseases caused by influenza viruses. They are
 CC also used as vaccines. The present sequence is equine influenza (ei)
 CC virus H3N8 Peical (cold adapted) NS230 protein which is encoded by
 CC neicalNS988 DNA
 XX
 SQ Sequence 230 AA;

Query Match 100.0%; Score 1178; DB 4; Length 230;
 Best Local Similarity 100.0%; Pred. No. 9.3e-118;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDSNTVSSFOVDCFLWHVRRKRFADQELGDAFLDLRLRRDQKSLKGRGSLGLDLETATRA 60
 DB 1 MDSNTVSSFOVDCFLWHVRRKRFADQELGDAFLDLRLRRDQKSLKGRGSLGLDLETATRA 60
 QY 61 GKQIVQIILEESDEALKNVTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
 DB 61 GKQIVQIILEESDEALKNVTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
 QY 121 QAIMDKNIIILKANFSVIFERLETLILRAFTTEGAVGEISPLPSLPGHTNEDVKNAIGV 180
 DB 121 QAIMDKNIIILKANFSVIFERLETLILRAFTTEGAVGEISPLPSLPGHTNEDVKNAIGV 180
 QY 181 LIGLKWNDNTVRISETLQRFARSSSHENGSRPSFPKQKRWERTIEPEV 230
 DB 181 LIGLKWNDNTVRISETLQRFARSSSHENGSRPSFPKQKRWERTIEPEV 230

RESULT 3
 AAW03522
 ID AAW03522 standard; protein; 230 AA.
 XX
 AC AAW03522;
 XX
 DT 16-OCT-2003 (revised)
 DT 09-APR-1997 (first entry)
 XX
 DE Non-structural protein NS1 of influenza A virus.
 XX
 KW Non-structural protein; NS1; influenza virus; respiratory tract;
 KW diagnosis; anti-NS1 antibody; primer; PCR; detection; amplify.
 XX
 OS Influenza virus; A/equine 1/Suffolk 89.
 XX
 PN EP726316-A2.
 XX
 PD 14-AUG-1996.
 XX
 PF 31-JAN-1996; 96EP-00300681.
 XX
 PR 09-FEB-1995; 95GB-00002489.
 XX
 PA (ANIM-) ANIMAL HEALTH TRUST.
 XX
 PI Binns M, Birch-Machin I;
 XX
 DR WPI: 1996-364394/37.
 DR N-PSDB; AAT37435.
 XX
 PT Recombinant equine influenza virus NS1 protein - useful for diagnosis of
 PT equine influenza A.
 XX
 PS Example; Fig 1A; 20pp; English.
 XX
 CC This sequence represents non-structural protein NS1 of influenza virus
 CC A/equine 2/Suffolk 89. The NS1 protein is useful for diagnosis of equine
 CC influenza A infections by detection of anti-NS1 antibodies. The NS1
 CC coding sequence was isolated using the primer sequences given in AAT37436
 CC -40.. (Updated on 16-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 230 AA;

Query Match 98.9%; Score 1165; DB 2; Length 230;
 Best Local Similarity 98.7%; Pred. No. 2.3e-116;
 Matches 227; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MDSNTVSSFOVDCFLWHVRRKRFADQELGDAFLDLRLRRDQKSLKGRGSLGLDLETATRA 60
 DB 1 MDSNTVSSFOVDCFLWHVRRKRFADQELGDAFLDLRLRRDQKSLKGRGSLGLDLETATRA 60

QY 61 GKQIVQEILEEESDEALKMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
DB 61 GKQIVQEILEEESDEAFKMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIILKANFSVIFERLETLILLRAFTEGAGVGEISPLPSLPCHTNEDEVKNAIGV 180
DB 121 QAIMDKNIILKANFSVIFERLETLILLRAFTEGAGVGEISPLPSLPCHTNEDEVKNAIGV 180
QY 181 LIGGLKWNNDTVRISETLQRFAMRSHENGSRPFPKQKRMERTIEPEV 230
DB 181 LIGGLKWNNDTVRVSETLQRFAMRSHENGSRPFPKQKRMERTIESEV 230
RESULT 4
AD014175
ID AD014175 standard; protein; 230 AA.
XX
AC AD014175;
XX
DT 12-AUG-2004 (first entry)
XX
DE Influenza A virus non-structural protein (NS)-1 #5.
XX
KW influenza inhibitor; influenza virus; non-structural protein-1; NS1;
KW double-stranded RNA; dsRNA; binding domain; virucide;
KW double-stranded-RNA-activated protein kinase; phosphorylation;
KW translation inhibition factor; eIF2alpha; viral protein synthesis;
KW viral protein replication; screening method; infection.
XX
OS Influenza A virus.
XX
PN WO2004043404-A2.
XX
PD 27-MAY-2004.
XX
PF 13-NOV-2003; 2003WO-US036292.
XX
PR 13-NOV-2002; 2002US-0425661P.
PR 10-JUN-2003; 2003US-0477453P.
XX
PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.
XX
PI Montelione GT, Krug RM;
XX
PI WPI; 2004-420083/39.
XX
DR
XX
CC This invention relates to a novel method of identifying an inhibitor of
CC influenza virus which comprises testing candidate compounds for their
CC ability to reduce the extent of binding between influenza virus non-
CC structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding
CC domain and a dsRNA that binds the protein. The invention may be useful
CC for the production of compounds with a virucide activity acting as
CC inhibitors of binding between influenza virus non-structural protein-1
CC (NS1) and double-stranded RNA. It is possible that binding of double-
CC stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA
CC -activated protein kinase to remain in an inactive state so that it does
CC not catalyze the phosphorylation of translation inhibition factor
CC eIF2alpha, which would otherwise inhibit viral protein synthesis and
CC replication. The invention is useful as a (high throughput) screening
CC method for identifying compounds having inhibitory activity against
CC influenza virus. Compounds identified are useful in treating animals,
CC including human infected with influenza virus. The present sequence is
CC that of an influenza virus non-structural (NS)-1 protein which is related
CC to the method of the invention.

SQ Sequence 230 AA;
Query Match 93.3%; Score 1099; DB:8; Length 230;
Best Local Similarity 92.6%; Pred. No. 2.9e-109;
Matches 213; Conservative 11; Mismatches 6; Indels 0; Gaps 0;
QY 1 MDSNTVSSSQVDCFLWHVYKRFADQELGDAPFLDLRRDQSKLGRGSTLGLDIETATRA 60
DB 1 MDSNTVSSSQVDCFLWHVYKRFADQELGDAPFLDLRRDQSKLGRGSTLGLDIETATCA 60
QY 61 GKQIVQEILEEESDEALKMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
DB 61 GKQIVQEILEEESDEALKMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIILKANFSVIFERLETLILLRAFTEGAGVGEISPLPSLPCHTNEDEVKNAIGV 180
DB 121 QAIMDKNIILKANFSVIFERLETLILLRAFTEGAGVGEISPLPSLPCHTNEDEVKNAIGV 180
QY 181 LIGGLKWNNDTVRISETLQRFAMRSHENGSRPFPKQKRMERTIEPEV 230
DB 181 LIGGLKWNNDTVRVSETLQRFAMRSHENGSRPFPKQKRMERTIESEV 230
RESULT 5
AD014179
ID AD014179 standard; protein; 227 AA.
XX
AC AD014179;
XX
DT 12-AUG-2004 (first entry)
XX
DE Influenza A virus non-structural protein (NS)-1 #9.
XX
KW influenza inhibitor; influenza virus; non-structural protein-1; NS1;
KW double-stranded RNA; dsRNA; binding domain; virucide;
KW double-stranded-RNA-activated protein kinase; phosphorylation;
KW translation inhibition factor; eIF2alpha; viral protein synthesis;
KW viral protein replication; screening method; infection.
XX
OS Influenza A virus.
XX
PN WO2004043404-A2.
XX
PD 27-MAY-2004.
XX
PF 13-NOV-2003; 2003WO-US036292.
XX
PR 13-NOV-2002; 2002US-0425661P.
PR 10-JUN-2003; 2003US-0477453P.
XX
PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.
XX
PI Montelione GT, Krug RM;
XX
PI WPI; 2004-420083/39.
XX
DR
XX
CC Identifying agents useful for treating influenza virus infection
CC comprises identifying compounds that inhibit binding between influenza
CC virus non-structural protein-1 (NS1) and a double-stranded RNA that binds
CC the protein.
XX
PS Disclosure; Page 13; 92pp; English.
XX
CC This invention relates to a novel method of identifying an inhibitor of
CC influenza virus which comprises testing candidate compounds for their
CC ability to reduce the extent of binding between influenza virus non-
CC structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding
CC domain and a dsRNA that binds the protein. The invention may be useful
CC for the production of compounds with a virucide activity acting as
CC inhibitors of binding between influenza virus non-structural protein-1
CC (NS1) and double-stranded RNA. It is possible that binding of double-
CC stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA
CC -activated protein kinase to remain in an inactive state so that it does

CC not catalyse the phosphorylation of translation inhibition factor
 CC eIF2alpha, which would otherwise inhibit viral protein synthesis and
 CC replication. The invention is useful as a (high throughput) screening
 CC method for identifying compounds having inhibitory activity against
 CC influenza virus. Compounds identified are useful in treating animals,
 CC including human infected with influenza virus. The present sequence is
 CC that of an influenza virus non-structural (NS)-1 protein which is related
 CC to the method of the invention.

SQ Sequence 227 AA;

Query March 91.9%; Score 1083; DB 8; Length 227;
 Best Local Similarity 92.1%; Pred. No. 1.5e-107; Indels 0; Gaps 0;
 Matches 209; Conservative 11; Mismatches 7;
 QY 4 NTVSSFOVDCFLMHWKRFADQELGDPFLDLRRDQSLGRGSLGLDIETATRAKQ 63
 DB 1 NTVSSFOVDCFLMHWKRFADQELGDPFLDLRRDQSLGRGSLGLDIETATRAKQ 60
 QY 64 IVFOILEESDEALQMTIASVPASRYLTDMTLDMSRDWFMMPKQVGTSLCIRMDQAI 123
 DB 61 IVERILVEESDEALQMTIASVPASRYLTDMTLDMSRDWFMMPKQVGTSLCIRMDQAI 120
 QY 124 MDKNIILKANFSVIFERLETLILLRAFTGEGAVGGEISPLPSLPGHTNEDVKNAIGVLIG 183
 DB 121 MDKNIILKANFSVIFERLETLILLRAFTGEGAVGGEISPLPSLPGHTNEDVKNAIGVLIG 180
 QY 184 GLKWNNTVRISETLQRPAMRSSHENGSRPFPKQKQKQRTIEPEV 230
 DB 181 GLEWNDNTVRVSETLQRPAMRSSNEDGRPLLPKQKQKQRTIEPEV 227

RESULT 6

AD014177
 ID AD014177 standard; protein; 227 AA.
 AC AD014177;
 DT 12-AUG-2004 (first entry)
 XX Influenza A virus non-structural protein (NS)-1 #7.
 XX influenza inhibitor; influenza virus; non-structural protein-1; NS1;
 KW double-stranded RNA; dsRNA; binding domain; virucide;
 KW double-stranded-RNA-activated protein kinase; phosphorylation;
 KW translation inhibition factor; eIF2alpha; viral protein synthesis;
 KW viral protein replication; screening method; infection.
 XX Influenza A virus.
 OS WO2004043404-A2.
 DX 27-MAY-2004.
 XX 13-NOV-2003; 2003WO-US036292.
 PF 13-NOV-2002; 2002US-0425661P.
 PR 10-JUN-2003; 2003US-0477453P.
 XX (RUTP) UNIV RUTGERS STATE NEW JERSEY.
 PA Montellione GT, Krug RM;
 XX WPI; 2004-420083/39.

Identifying agents useful for treating influenza virus infection
 comprises identifying compounds that inhibit binding between influenza
 PT virus non-structural protein-1 (NS1) and a double-stranded RNA that binds
 PT the protein.

Disclosure; Page 13; 92pp; English.

This invention relates to a novel method of identifying an inhibitor of

CC influenza virus which comprises testing candidate compounds for their
 CC ability to reduce the extent of binding between influenza virus non-
 CC structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding
 CC domain and a dsRNA that binds the protein. The invention may be useful
 CC for the production of compounds with a virucide activity acting as
 CC inhibitors of binding between influenza virus non-structural protein-1
 CC (NS1) and double-stranded RNA. It is possible that binding of double-
 CC stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA
 CC -activated protein kinase to remain in an inactive state so that it does
 CC not catalyse the phosphorylation of translation inhibition factor
 CC eIF2alpha, which would otherwise inhibit viral protein synthesis and
 CC replication. The invention is useful as a (high throughput) screening
 CC method for identifying compounds having inhibitory activity against
 CC influenza virus. Compounds identified are useful in treating animals,
 CC including human infected with influenza virus. The present sequence is
 CC that of an influenza virus non-structural (NS)-1 protein which is related
 CC to the method of the invention.

SQ Sequence 227 AA;

Query March 90.5%; Score 1066; DB 8; Length 227;
 Best Local Similarity 91.2%; Pred. No. 1e-105; Indels 0; Gaps 0;
 Matches 207; Conservative 11; Mismatches 9;
 QY 4 NTVSSFOVDCFLMHWKRFADQELGDPFLDLRRDQSLGRGSLGLDIETATRAKQ 63
 DB 1 NTVSSFOVDCFLMHWKRFADQELGDPFLDLRRDQSLGRGSLGLDIETATRAKQ 60
 QY 64 IVEOILEESDEALQMTIASVPASRYLTDMTLDMSRDWFMMPKQVGTSLCIRMDQAI 123
 DB 61 IVERILVEESDEALQMTIASVPASRYLTDMTLDMSRDWFMMPKQVGTSLCIRMDQAI 120
 QY 124 MDKNIILKANFSVIFERLETLILLRAFTGEGAVGGEISPLPSLPGHTNEDVKNAIGVLIG 183
 DB 121 MDKNIILKANFSVIFERLETLILLRAFTGEGAVGGEISPLPSLPGHTNEDVKNAIGVLIG 180
 QY 184 GLKWNNTVRISETLQRPAMRSSHENGSRPFPKQKQKQRTIEPEV 230
 DB 181 GLEWNDNTVRVSETLQRPAMRSSNEDGRPLLPKQKQKQRTIEPEV 227

RESULT 7

AD014174
 ID AD014174 standard; protein; 230 AA.
 AC AD014174;
 DT 12-AUG-2004 (first entry)
 XX Influenza A virus non-structural protein (NS)-1 #4.
 XX influenza inhibitor; influenza virus; non-structural protein-1; NS1;
 KW double-stranded RNA; dsRNA; binding domain; virucide;
 KW double-stranded-RNA-activated protein kinase; phosphorylation;
 KW translation inhibition factor; eIF2alpha; viral protein synthesis;
 KW viral protein replication; screening method; infection.
 XX Influenza A virus.
 OS WO2004043404-A2.
 DX 27-MAY-2004.
 XX 13-NOV-2003; 2003WO-US036292.
 PF 13-NOV-2002; 2002US-0425661P.
 PR 10-JUN-2003; 2003US-0477453P.
 XX (RUTP) UNIV RUTGERS STATE NEW JERSEY.
 PA Montellione GT, Krug RM;
 XX WPI; 2004-420083/39.

XX Identifying agents useful for treating influenza virus infection
 PT comprises identifying compounds that inhibit binding between influenza
 PT virus non-structural protein-1 (NS1) and a double-stranded RNA that binds
 PT the protein.

XX Disclosure; Page 12; 92pp; English.

XX This invention relates to a novel method of identifying an inhibitor of
 CC influenza virus which comprises testing candidate compounds for their
 CC ability to reduce the extent of binding between influenza virus non-
 CC structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding
 CC domain and a dsRNA that binds the protein. The invention may be useful
 CC for the production of compounds with a virucide activity acting as
 CC inhibitors of binding between influenza virus non-structural protein-1
 CC (NS1) and double-stranded RNA. It is possible that binding of double-
 CC stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA
 CC -activated protein kinase to remain in an inactive state so that it does
 CC not catalyze the phosphorylation of translation inhibition factor
 CC eIF2alpha, which would otherwise inhibit viral protein synthesis and
 CC replication. The invention is useful as a (high throughput) screening
 CC method for identifying compounds having inhibitory activity against
 CC influenza virus. Compounds identified are useful in treating animals,
 CC including human infected with influenza virus. The present sequence is
 CC that of an influenza virus non-structural (NS)-1 protein which is related
 CC to the method of the invention.

XX Sequence 230 AA;

Query Match 90.5%; Score 1066; DB 8; Length 230;
 Best Local Similarity 90.0%; Pred. No. 1e-105;
 Matches 207; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
 QY 1 MDSNTVSSQVDCFLMHWVRKFADELDGAPFLDRLDQKSLKGRGSLGLDITATRA 60
 DB 1 MDSNTVSSQVDCFLMHWVRKFADELDGAPFLDRLDQKSLKGRGSLGLDITATRA 60
 QY 61 GKQIVQILEESDEALKMTIASVPASRYLTDMTLDEMGRDWFMLMPKQKVTGSLCIRMD 120
 DB 61 GKQIVQILEESDEALKMTIASVPASRYLTDMTLDEMGRDWFMLMPKQKVTGSLCIRMD 120
 QY 121 QAIMDKNIIILKANFSVIFERLETLILRAFTPEGAVGEISPLSPGHTNEDVKNATGV 180
 DB 121 QAIMDKNIIILKANFSVIFERLETLILRAFTPEGAVGEISPLSPGHTNEDVKNATGV 180
 QY 181 LIGGLKWNNDTVRISETLQRFAMWSSHENGSRPSPPPKQKRMKERTIEPEV 230
 DB 181 LIGGLEWNDNTVRDSETLQRFAMWSSHENGSRPSPPPKQKRMKERTIESEV 230

RESULT 8

ADY62119
 ID ADY62119 standard; protein; 238 AA.

XX AC ADY62119;

XX 19-MAY-2005 (first entry)

XX Influenza A virus strain A/England/1/53 wild type NS1 protein.

XX protein engineering; immune stimulation; immunostimulant; vaccine;
 KW influenza virus infection.

XX Influenza A virus; strain A/England/1/53.

XX US2005054846-A1.

XX 10-MAR-2005.

XX 04-SEP-2003; 2003US-00654737.

XX 04-SEP-2003; 2003US-00654737.

PA (WEBB/) WEBSTER R G.
 PA (WEBB/) WEBBY R J.
 XX (OZAK/) OZAKI H.

PI Webster RG, Webby RJ, Ozaki H;

DR WPI: 2005-213104/22.
 DR N-PSDB; ADY62117.

PT Producing a reassortant influenza virus that gives a high titer in Vero
 PT cells (certified for use in vaccine-production), comprises replacing the
 PT NS gene of the A/PuertoRico/3/24 master strain with the NS gene of the
 PT A/England/1/53 strain.

XX Claim 2; SEQ ID NO 3; 16pp; English.

XX The invention relates to a method of producing a high titer reassortant
 CC influenza virus by transfecting host cells with expression plasmids
 CC containing the PB2, PB1, PA, NP, and M genes from the A/PuertoRico/8/34
 CC influenza strain, the NS gene from the A/England/1/53 influenza strain,
 CC and the HA and NA genes from an influenza virus of interest other than
 CC A/England/1/53, to obtain a high titer reassortant influenza virus. The
 CC method is useful for producing a high titer reassortant influenza virus.
 CC The high titer reassortant influenza viruses are useful for producing
 CC vaccine compositions. The vaccines are useful for treating or preventing
 CC influenza viral infections. Genetic engineering techniques allow the
 CC rapid production of custom made attenuated virus vaccines, but vaccine
 CC use is limited by the need to use vaccine approved cell lines. The master
 CC strain A/PuertoRico/8/34 which is the most widely used in producing
 CC recombinant viruses for vaccine use produces a high titer in MDCK cells,
 CC which are not certified for use in production of human vaccines, but not
 CC in Vero cells, which are certified for this use. The applicants have
 CC discovered that replacing the NS gene of the A/PuertoRico/3/24 master
 CC strain with the NS gene of the A/England/1/53 strain gives reassortant
 CC virus that produces a high titer in Vero cells. This sequence corresponds
 CC to the NS1 protein from the A/England/1/53 influenza strain.

XX Sequence 238 AA;

Query Match 90.18; Score 1061; DB 9; Length 238;
 Best Local Similarity 88.7%; Pred. No. 3.7e-105;
 Matches 204; Conservative 14; Mismatches 12; Indels 0; Gaps 0;
 QY 1 MDSNTVSSQVDCFLMHWVRKFADELDGAPFLDRLDQKSLKGRGSLGLDITATRA 60
 DB 1 MDSNTVSSQVDCFLMHWVRKFADELDGAPFLDRLDQKSLKGRGSLGLDITATRA 60
 QY 61 GKQIVQILEESDEALKMTIASVPASRYLTDMTLDEMGRDWFMLMPKQKVTGSLCIRMD 120
 DB 61 GKQIVQILEESDEALKMTIASVPASRYLTDMTLDEMGRDWFMLMPKQKVTGSLCIRMD 120
 QY 121 QAIMDKNIIILKANFSVIFERLETLILRAFTPEGAVGEISPLSPGHTNEDVKNATGV 180
 DB 121 QAIMDKNIIILKANFSVIFERLETLILRAFTPEGAVGEISPLSPGHTNEDVKNATGV 180
 QY 181 LIGGLKWNNDTVRISETLQRFAMWSSHENGSRPSPPPKQKRMKERTIEPEV 230
 DB 181 LIGGLEWNDNTVRVSKTLQRFAMWSSHENGSRPSPPPKQKRMKERTIRSEV 230

RESULT 9

ADY62119
 ID ADY62119 standard; protein; 230 AA.

XX AC ADY62119;

XX 12-AUG-2004 (first entry)

XX Influenza A virus non-structural protein (NS)-1 #13.

XX influenza inhibitor; influenza virus; non-structural protein-1; NS1;

XX double-stranded RNA; dsRNA; binding domain; virucide; phosphorylation;
 KW double-stranded-RNA-activated protein kinase; phosphorylation;

XX DT 19-MAY-2005 (first entry)

XX DE Mutant Influenza A virus strain A/England/1/53v-a NS1 protein.

XX KW protein engineering; immune stimulation; immunostimulant; vaccine;

XX KW Influenza virus infection; mutin.

XX OS Influenza A virus; strain A/England/1/53v-a.

XX FH Key Location/Qualifiers

XX FT Misc-difference 21

XX FT FT /note= "replaces Gln in wild type protein"

XX FT FT Misc-difference 58

XX FT FT /note= "replaces Thr in wild type protein"

XX FT FT Misc-difference 60

XX FT FT /note= "replaces Val in wild type protein"

XX FT FT Misc-difference 127

XX FT FT /note= "replaces Asn in wild type protein"

XX FT FT Misc-difference 174

XX FT FT /note= "replaces Val in wild type protein"

XX FT FT Misc-difference 189

XX FT FT /note= "replaces Asp in wild type protein"

XX PN US2005054846-A1.

XX PD 10-MAR-2005.

XX PF 04-SEP-2003; 2003US-00654737.

XX PR 04-SEP-2003; 2003US-00654737.

XX PA (WEBSTER) WEBSTER R G.

XX PA (WEBB) WEBB R J.

XX PA (OZAKI) OZAKI H.

XX PI Webster RG, Webby RJ, Ozaki H;

XX PN WPI: 2005-213104/22.

XX DR N-PSDB; ADY62118.

XX XX Producing a reassortant influenza virus that gives a high titer in Vero cells (certified for use in vaccine-production), comprises replacing the NS gene of the A/PuertoRico/3/24 master strain with the NS gene of the A/England/1/53 strain.

XX PS Claim 6; SEQ ID NO 5; 16pp; English.

XX CC The invention relates to a method of producing a high titer reassortant influenza virus by transfecting host cells with expression plasmids containing the PB2, PB1, PA, NP, and M genes from the A/PuertoRico/9/34 influenza strain, the NS gene from the A/England/1/53 influenza strain, and the HA and NA genes from an influenza virus of interest other than A/England/1/53, to obtain a high titer reassortant influenza virus. The method is useful for producing a high titer reassortant influenza virus. The high titer reassortant influenza viruses are useful for producing vaccine compositions. The vaccines are useful for treating or preventing influenza viral infections. Genetic engineering techniques allow the rapid production of custom made attenuated virus vaccines, but vaccine use is limited by the need to use vaccine approved cell lines. The master strain A/PuertoRico/8/34 which is the most widely used in producing recombinant viruses for vaccine use produces a high titer in MDCK cells, which are not certified for use in production of human vaccines, but not in Vero cells, which are certified for this use. The applicants have discovered that replacing the NS gene of the A/PuertoRico/3/24 master strain with the NS gene of the A/England/1/53 strain gives reassortant virus that produces a high titer in Vero cells. This sequence corresponds to the mutated NS1 protein from the A/England/1/53v-a influenza strain.

XX CC Sequence 230 AA;

Query Match 89.3%; Score 1052; DB 9; Length 230;

Best Local Similarity 87.8%; Pred. No. 3.3e-104;

Matches 202; Conservative 16; Mismatches 12; Indels 0; Gaps 0;

QY 1 MDNTVSSFOVDCFLWVRKRPADQELGADPDLRLRRDOKSLKGRGSLGLDITATRA 60

DB 1 MDNTVSSFOVDCFLWVRKRPADQELGADPDLRLRRDOKSLKGRGSLGLDITATRA 60

QY 61 GKQIVBOILEESDEALKMTIASVPASRYLTDMTLDEMSDFWMLPKQKVTGSLCIRMD 120

DB 61 GKQIVBOILEESDEALKMTIASVPASRYLTDMTLDEMSDFWMLPKQKVTGSLCIRMD 120

QY 121 QATMDKNILKANFSVIFEELETLILLRAFTEEGAVVEISPLSPGHTNEDVNAIGV 180

DB 121 QATMDKNILKANFSVIFEELETLILLRAFTEEGAVVEISPLSPGHTNEDVNAIGV 180

QY 181 LIGGLKNDVTVRISETLORFWRSHENGRSPFPKQKMERETIEPY 230

DB 181 LIGGLEWNNVTVRSKTLQRFWRSHENGRSPFPKQKMERETIEPY 230

RESULT 12

ID ADO14180 standard; protein; 227 AA.

XX AC ADO14180;

XX DT 12-AUG-2004 (first entry)

XX DE Influenza A virus non-structural protein (NS)-1 #10.

XX KW influenza inhibitor; influenza virus; non-structural protein-1; NS1;

XX KW double-stranded RNA; dsRNA; binding domain; virucide;

XX KW double-stranded-RNA-activated protein kinase; phosphorylation;

XX KW translation inhibition factor; eIF2alpha; viral protein synthesis;

XX KW viral protein replication; screening method; infection.

XX OS Influenza A virus.

XX PN WO2004043404-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036292.

XX PR 13-NOV-2002; 2002US-0425661P.

XX PR 10-JUN-2003; 2003US-0477453P.

XX PA (RUTP) UNIV RUTGERS STATE NEW JERSEY.

XX PI Montelione GT, Krug RM;

XX DR WPI; 2004-420083/39.

XX PT Identifying agents useful for treating influenza virus infection comprises identifying compounds that inhibit binding between influenza virus non-structural protein-1 (NS1) and a double-stranded RNA that binds the protein.

XX PS Disclosure; Page 13-14; 92pp; English.

XX CC This invention relates to a novel method of identifying an inhibitor of influenza virus which comprises testing candidate compounds for their ability to reduce the extent of binding between influenza virus non-structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding domain and a dsRNA that binds the protein. The invention may be useful for the production of compounds with a virucide activity acting as inhibitors of binding between influenza virus non-structural protein-1 (NS1) and double-stranded RNA. It is possible that binding of double-stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA-activated protein kinase to remain in an inactive state so that it does not catalyze the phosphorylation of translation inhibition factor eIF2alpha, which would otherwise inhibit viral protein synthesis and replication. The invention is useful as a (high throughput) screening method for identifying compounds having inhibitory activity against

CC influenza virus. Compounds identified are useful in treating animals,
CC including human infected with influenza virus. The present sequence is
CC that of an influenza virus non-structural (NS)-1 protein which is related
CC to the method of the invention.

XX SQ Sequence 227 AA;

Query Match 89.2%; Score 1051; DB 8; Length 227;
Best Local Similarity 90.3%; Pred. No. 4.1e-104; Indels 0; Gaps 0;
Matches 205; Conservative 8; Mismatches 14; Indels 0; Gaps 0;
QY 4 NTVSSFOVDCFLWHVYKRFADQELGDPFLDRLRRDOKSLKGRSTGLDLETATRAKQ 63
DB 1 NTVSSFOVDCFLWHVYKRFADQELGDPFLDRLRRDOKSLKGRSTGLDLETATRAKQ 60
QY 64 IVKQILKEESDEALKWTIASVPASRYLTDMTLDMSRDWFLMPKQKVTGSLCIRMDQAI 123
DB 61 IVKQILKEESDEALKWTIASVPASRYLTDMTLDMSRDWFLMPKQKVTGSLCIRMDQAI 120
QY 124 MDKXNIIILKANFSVIFERLETLILRAFTTEGAIVGEISPLSPGHTNEDVKNAGVILIG 183
DB 121 MDKXNIIILKANFSVIFERLETLILRAFTTEGAIVGEISPLSPGHTNEDVKNAGVILIG 180
QY 184 GLKWNNTVRISSETLQRFAMRSSHENGSRFPFPKQKQKMERITIEEV 230
DB 181 GLEWNTVRSVSETLQRFAMRSSHENGSRFPFPKQKQKMERITIEEV 227

RESULT 13
AD014171
ID AD014171 standard; protein; 230 AA.
XX AC AD014171;
XX DT 12-AUG-2004 (first entry)
XX DE Influenza A virus non-structural protein (NS)-1 #1.
XX KW influenza inhibitor; influenza virus; non-structural protein-1; NS1;
KW double-stranded RNA; dsRNA; binding domain; virucide;
KW double-stranded RNA-activated protein kinase; phosphorylation;
KW translation inhibition factor; eIF2alpha; viral protein synthesis;
KW viral protein replication; screening method; infection.
XX OS Influenza A virus; A/Udorn/307/72 (H3N2).
XX PN WO2004043404-A2.
XX PD 27-MAY-2004.
XX PF 13-NOV-2003; 2003WO-US036292.
XX PR 13-NOV-2002; 2002US-0425661P.
XX PR 10-JUN-2003; 2003US-0477453P.
XX PA (RUTP) UNIV RUTGERS STATE NEW JERSEY.
XX PI Montellione GT, Krug RM;
XX DT 27-MAY-2004.
XX DR WPI; 2004-420083/39.
XX PT Identifying agents useful for treating influenza virus infection
PT comprises identifying compounds that inhibit binding between influenza
PT virus non-structural protein-1 (NS1) and a double-stranded RNA that binds
PT the protein.

XX PS Disclosure; Page 11; 92pp; English.
XX CC This invention relates to a novel method of identifying an inhibitor of
CC influenza virus which comprises testing candidate compounds for their
CC ability to reduce the extent of binding between influenza virus non-
CC structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding
CC domain and a dsRNA that binds the protein. The invention may be useful

CC for the production of compounds with a virucide activity acting as
CC inhibitors of binding between influenza virus non-structural protein-1
CC (NS1) and double-stranded RNA. It is possible that binding of double-
CC stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA
CC -activated protein kinase to remain in an inactive state so that it does
CC not catalyze the phosphorylation of translation inhibition factor
CC eIF2alpha, which would otherwise inhibit viral protein synthesis and
CC replication. The invention is useful as a (high throughput) screening
CC method for identifying compounds having inhibitory activity against
CC influenza virus. Compounds identified are useful in treating animals,
CC including human infected with influenza virus. The present sequence is
CC that of an influenza virus non-structural (NS)-1 protein which is related
CC to the method of the invention.

XX SQ Sequence 230 AA;
Query Match 89.0%; Score 1048; DB 8; Length 230;
Best Local Similarity 88.3%; Pred. No. 8.8e-104;
Matches 203; Conservative 14; Mismatches 13; Indels 0; Gaps 0;
QY 1 MDSNTVSSFOVDCFLWHVYKRFADQELGDPFLDRLRRDOKSLKGRSTGLDLETATRA 60
DB 1 MDPNTVSSFOVDCFLWHVYKRFADQELGDPFLDRLRRDOKSLKGRSTGLDLETATRA 60
QY 61 GKQIVEITKEESDEALKWTIASVPASRYLTDMTLDMSRDWFLMPKQKVTGSLCIRMD 120
DB 61 GKQIVEITKEESDEALKWTIASVPASRYLTDMTLDMSRDWFLMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIIILKANFSVIFERLETLILRAFTTEGAIVGEISPLSPGHTNEDVKNAGV 180
DB 121 QAIMDKNIIILKANFSVIFERLETLILRAFTTEGAIVGEISPLSPGHTNEDVKNAGV 180
QY 181 LIGGLKWNNTVRISSETLQRFAMRSSHENGSRFPFPKQKQKMERITIEEV 230
DB 181 LIGGLEWNTVRSVSETLQRFAMRSSHENGSRFPFPKQKQKMERITIEEV 230

RESULT 14
AD014176
ID AD014176 standard; protein; 230 AA.
XX AC AD014176;
XX DT 12-AUG-2004 (first entry)
XX DE Influenza A virus non-structural protein (NS)-1 #6.
XX KW influenza inhibitor; influenza virus; non-structural protein-1; NS1;
KW double-stranded RNA; dsRNA; binding domain; virucide;
KW double-stranded RNA-activated protein kinase; phosphorylation;
KW translation inhibition factor; eIF2alpha; viral protein synthesis;
KW viral protein replication; screening method; infection.
XX OS Influenza A virus.
XX PN WO2004043404-A2.
XX PD 27-MAY-2004.
XX PF 13-NOV-2003; 2003WO-US036292.
XX PR 13-NOV-2002; 2002US-0425661P.
XX PR 10-JUN-2003; 2003US-0477453P.
XX PA (RUTP) UNIV RUTGERS STATE NEW JERSEY.
XX PI Montellione GT, Krug RM;
XX DT 27-MAY-2004.
XX DR WPI; 2004-420083/39.
XX PT Identifying agents useful for treating influenza virus infection
PT comprises identifying compounds that inhibit binding between influenza
PT virus non-structural protein-1 (NS1) and a double-stranded RNA that binds

PT the protein.
 XX Disclosure; Page 12-13; 92pp; English.
 XX This invention relates to a novel method of identifying an inhibitor of
 CC influenza virus which comprises testing candidate compounds for their
 CC ability to reduce the extent of binding between influenza virus non-
 CC structural protein-1 (NS1) or its double-stranded RNA (dsRNA) binding
 CC domain and a dsRNA that binds the protein. The invention may be useful
 CC for the production of compounds with a virucide activity acting as
 CC inhibitors of binding of compounds with influenza virus non-structural protein-1
 CC (NS1) and double-stranded RNA. It is possible that binding of double-
 CC stranded RNA by the NS1 protein in a host cell causes double-stranded-RNA
 CC activated protein kinase to remain in an inactive state so that it does
 CC not catalyze the phosphorylation of translation inhibition factor and
 CC eIF2alpha, which would otherwise inhibit viral protein synthesis and
 CC replication. The invention is useful as a high throughput screening
 CC method for identifying compounds having inhibitory activity against
 CC influenza virus. Compounds identified are useful in treating animals,
 CC including human infected with influenza virus. The present sequence is
 CC that of an influenza virus non-structural (NS)-1 protein which is related
 CC to the method of the invention.

XX Sequence 230 AA;
 SQ

Query Match 88.5%; Score 1042; DB 8; Length 230;
 Best Local Similarity 87.8%; Pred. No. 3.9e-103;
 Matches 202; Conservative 16; Mismatches 12; Indels 0; Gaps 0;
 QY 1 MDSNTVSSFDVDCFLMHWVRKRFADQELGDAPFLDRLRDQKSLKRGSTGLGDIETATRA 60
 DB 1 MDSNTVSSFDVDCFLMHWVRKRFADQELGDAPFLDRLRDQKSLKRGSTGLGDIETATRA 60
 QY 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMTLDMSRDWFLMPKQKVTGSLCIRMD 120
 DB 61 GKQIVERILEESNEALKMTIASVPASRYLTDMTLEMSRDWFLMPKQKVGSLCIRMD 120
 QY 121 QAIMDKNIILKANFSVIFERLETLILLRAFTTEGAVVGEISPLPSLPGHTNEDVKNAGV 180
 DB 121 QALMEKSIILKANFSVIFDRLETLILLRAFTTEGAVVGEISPLPSLPGHTNEDVKNAGV 180
 QY 181 LIGGLKWNNDTVRISSETLQRFWRSSHENGSRPSPKPKKQKERTIEPEV 230
 DB 181 LIGGLEWNGNTVRVSENLORFWRSSNENRSLPPKPKKQREVACTIRSEV 230

RESULT 15
 ABB05772

ID ABB05772 standard; protein; 237 AA.

XX AC ABB05772;

XX DT 07-MAY-2002 (first entry)

XX DE Influenza A/Udorn/72 (H3N2) Strain NS1 protein SEQ ID NO:18.

XX KW Influenza A/Udorn/72 (H3N2) strain; Influenzavirus A; diagnosis;

XX KW Influenza A virus; genome.

XX OS Influenzavirus A.

XX PN WO200200884-A2.

XX PD 03-JAN-2002.

XX PF 21-JUN-2001; 2001WO-US019826.

XX PR 23-JUN-2000; 2000US-0213650P.

XX PA (AMCY) AMERICAN CYANAMID CO.

XX PI Galarza JM, Latham TE;

DR WPI; 2002-139923/18.
 XX N-PSDB; ABA93942.
 PT Polynucleotide encoding complete sequence of influenza A/Udorn/72 and
 PT polypeptide, useful in diagnosis and for generating new Influenza A
 XX variant strains.
 PS Disclosure; Page 78-79; 103pp; English.
 XX The present invention describes an isolated polynucleotide (I) having the
 CC complete sequence of the Influenza A/Udorn/72 (H3N2) strain in positive
 CC strand, and genomic message sense. ABA93934 to ABA93944 encode the
 CC Influenza A/Udorn/72 (H3N2) strain protein given in ABB05764 to ABB05774
 CC from the present invention. (I) is useful for designing polymerase chain
 CC reaction (PCR) primers for use in a PCR assay to detect the presence of
 CC the corresponding virus segment in a sample or for designing and
 CC selecting peptides for use in an enzyme linked immunosorbent assay to
 CC detect the presence of the corresponding protein produced by that segment
 CC in a sample, hence is useful in diagnosis and may be modified by mutation
 CC to generate new Influenza A variant strains. ABA94945 to ABA94939
 CC represent Influenza A/Udorn/72 (H3N2) strain sequencing primers, which
 CC are used in an example from the present invention

XX Sequence 237 AA;
 SQ

Query Match 85.7%; Score 1010; DB 5; Length 237;
 Best Local Similarity 83.9%; Pred. No. 1.1e-99;
 Matches 193; Conservative 19; Mismatches 18; Indels 0; Gaps 0;
 QY 1 MDSNTVSSFDVDCFLMHWVRKRFADQELGDAPFLDRLRDQKSLKRGSTGLGDIETATRA 60
 DB 1 MDSNTVSSFDVDCFLMHWVRKRFADQELGDAPFLDRLRDQKSLKRGSTGLGDIETATRA 60
 QY 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMTLDMSRDWFLMPKQKVTGSLCIRMD 120
 DB 61 GKQIVEKILKEESDEALKMTMTASTPASRYITDMTIELSRDWFLMPKQKVEGFLCIRID 120
 QY 121 QAIMDKNIILKANFSVIFERLETLILLRAFTTEGAVVGEISPLPSLPGHTNEDVKNAGV 180
 DB 121 QAIMDKNIILKANFSVIFDRLETLILLRAFTTEGAVVGEISPLPSLPGHTTIEDVKNAGV 180
 QY 181 LIGGLKWNNDTVRISSETLQRFWRSSHENGSRPSPKPKKQKERTIEPEV 230
 DB 181 LIGGLEWNGNTVRVSKTLQRFWRSSNENRPLTPKPKKQKQKARTARSKV 230

Search completed: March 7, 2006, 19:17:07
 Job time : 188 secs

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RESULT 2
Q9YJ2 9INFA
ID Q9YJ2 9INFA PRELIMINARY; PRT; 230 AA.
AC Q9YJ2;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nonstructural protein NS1
OS Influenza A virus (A/eq/Kentucky/92 (H3N8))
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=60025;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98411653; PubMed=9739336; DOI=10.1007/s007050050400;
RA Lindstrom S., Endo A., Sugita S., Pecoraro M., Hiromoto Y., Kanada M.,
RA Takahashi T., Nerome K.;
RT "Phylogenetic analyses of equine influenza M and NS genes and
RT comparison with the HA gene.";
RL Arch. Virol. 143:1585-1598 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lindstrom S.E.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF001671; AAC31266.1; -, Genomic_RNA.
DR HSSP; P03495; 1-70.
DR SMR; Q9YJ2; 1-70.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000256; Flu_NS1.
DR Pfam; PF00600; Flu_NS1; 1.
DR ProDom; PD000613; Flu_NS1; 1.
SQ SEQUENCE 230 AA; 26169 MW; 8CCE20B9A6CAC2E6 CRC64;

Query Match 100.0%; Score 1178; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 4.8e-91;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSNTVSSFQVDCFLWHVYKRFADQELGDAFLDLRLRDQKSLKGRGSLGLDIETATRA 60
DB 1 MDSNTVSSFQVDCFLWHVYKRFADQELGDAFLDLRLRDQKSLKGRGSLGLDIETATRA 60
QY 61 GKQIVEQLLEESDEALAKWTIASVPASRYLTDMTLDMSRDWFMFMPKQKVTGSLCIRMD 120
DB 61 GKQIVEQLLEESDEALAKWTIASVPASRYLTDMTLDMSRDWFMFMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIIKANFSVIFERLETLILRAFTGEGAVGVEISPLSPFGHTNEDVKNAIGV 180
DB 121 QAIMDKNIIKANFSVIFERLETLILRAFTGEGAVGVEISPLSPFGHTNEDVKNAIGV 180
QY 181 LIGLKWNDNTVRISETLQRFANRSHENGSRPSFPKQKRWERTIEPEV 230
DB 181 LIGLKWNDNTVRISETLQRFANRSHENGSRPSFPKQKRWERTIEPEV 230

Query Match 100.0%; Score 1178; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 4.8e-91;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSNTVSSFQVDCFLWHVYKRFADQELGDAFLDLRLRDQKSLKGRGSLGLDIETATRA 60
DB 1 MDSNTVSSFQVDCFLWHVYKRFADQELGDAFLDLRLRDQKSLKGRGSLGLDIETATRA 60
QY 61 GKQIVEQLLEESDEALAKWTIASVPASRYLTDMTLDMSRDWFMFMPKQKVTGSLCIRMD 120
DB 61 GKQIVEQLLEESDEALAKWTIASVPASRYLTDMTLDMSRDWFMFMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIIKANFSVIFERLETLILRAFTGEGAVGVEISPLSPFGHTNEDVKNAIGV 180
DB 121 QAIMDKNIIKANFSVIFERLETLILRAFTGEGAVGVEISPLSPFGHTNEDVKNAIGV 180
QY 181 LIGLKWNDNTVRISETLQRFANRSHENGSRPSFPKQKRWERTIEPEV 230
DB 181 LIGLKWNDNTVRISETLQRFANRSHENGSRPSFPKQKRWERTIEPEV 230

RESULT 3
Q9Y268 9INFA
ID Q9Y268 9INFA PRELIMINARY; PRT; 230 AA.
AC Q9Y268;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nonstructural protein NS1
OS Influenza A virus (A/eq/Laplata/93 (H3N8))
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=60027;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98411653; PubMed=9739336; DOI=10.1007/s007050050400;
RA Lindstrom S., Endo A., Sugita S., Pecoraro M., Hiromoto Y., Kanada M.,
RA Takahashi T., Nerome K.;
RT "Phylogenetic analyses of equine influenza M and NS genes and
RT comparison with the HA gene.";
RL Arch. Virol. 143:1585-1598 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lindstrom S.E.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF001666; AAC31256.1; -, Genomic_RNA.
DR HSSP; P03495; 1-70.
DR SMR; Q9Y268; 1-70.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000256; Flu_NS1.
DR Pfam; PF00600; Flu_NS1; 1.
DR ProDom; PD000613; Flu_NS1; 1.
SQ SEQUENCE 230 AA; 26155 MW; 8CCE20E9B572F976 CRC64;

Query Match 99.9%; Score 1177; DB 2; Length 230;
Best Local Similarity 99.6%; Pred. No. 5.8e-91;
Matches 229; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSNTVSSFQVDCFLWHVYKRFADQELGDAFLDLRLRDQKSLKGRGSLGLDIETATRA 60
DB 1 MDSNTVSSFQVDCFLWHVYKRFADQELGDAFLDLRLRDQKSLKGRGSLGLDIETATRA 60
QY 61 GKQIVEQLLEESDEALAKWTIASVPASRYLTDMTLDMSRDWFMFMPKQKVTGSLCIRMD 120
DB 61 GKQIVEQLLEESDEALAKWTIASVPASRYLTDMTLDMSRDWFMFMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIIKANFSVIFERLETLILRAFTGEGAVGVEISPLSPFGHTNEDVKNAIGV 180
DB 121 QAIMDKNIIKANFSVIFERLETLILRAFTGEGAVGVEISPLSPFGHTNEDVKNAIGV 180
QY 181 LIGLKWNDNTVRISETLQRFANRSHENGSRPSFPKQKRWERTIEPEV 230
DB 181 LIGLKWNDNTVRISETLQRFANRSHENGSRPSFPKQKRWERTIEPEV 230

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Arch. Virol. 143:1585-1598 (1998).
RL [2]
RN NUCLEOTIDE SEQUENCE.
RP Lindstrom S.E.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF001673; AAC31270.1; -, Genomic_RNA.
DR HSSP; P03495; 1-70.
DR SMR; Q9Y268; 1-70.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000256; Flu_NS1.
DR Pfam; PF00600; Flu_NS1; 1.
DR ProDom; PD000613; Flu_NS1; 1.
SQ SEQUENCE 230 AA; 26155 MW; 746CAAD835D96965 CRC64;

Query Match 99.9%; Score 1177; DB 2; Length 230;
Best Local Similarity 99.6%; Pred. No. 5.8e-91;
Matches 229; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSNTVSSFQVDCFLWHVYKRFADQELGDAFLDLRLRDQKSLKGRGSLGLDIETATRA 60
DB 1 MDSNTVSSFQVDCFLWHVYKRFADQELGDAFLDLRLRDQKSLKGRGSLGLDIETATRA 60
QY 61 GKQIVEQLLEESDEALAKWTIASVPASRYLTDMTLDMSRDWFMFMPKQKVTGSLCIRMD 120
DB 61 GKQIVEQLLEESDEALAKWTIASVPASRYLTDMTLDMSRDWFMFMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIIKANFSVIFERLETLILRAFTGEGAVGVEISPLSPFGHTNEDVKNAIGV 180
DB 121 QAIMDKNIIKANFSVIFERLETLILRAFTGEGAVGVEISPLSPFGHTNEDVKNAIGV 180
QY 181 LIGLKWNDNTVRISETLQRFANRSHENGSRPSFPKQKRWERTIEPEV 230
DB 181 LIGLKWNDNTVRISETLQRFANRSHENGSRPSFPKQKRWERTIEPEV 230

RESULT 4
Q9Y272 9INFA
ID Q9Y272 9INFA PRELIMINARY; PRT; 230 AA.
AC Q9Y272;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nonstructural protein NS1
OS Influenza A virus (A/equine/Yvelines/2136/89 (H3N8))
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=225091;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98411653; PubMed=9739336; DOI=10.1007/s007050050400;
RA Lindstrom S., Endo A., Sugita S., Pecoraro M., Hiromoto Y., Kanada M.,
RA Takahashi T., Nerome K.;
RT "Phylogenetic analyses of equine influenza M and NS genes and
RT comparison with the HA gene.";
RL Arch. Virol. 143:1585-1598 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lindstrom S.E.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF001666; AAC31256.1; -, Genomic_RNA.
DR HSSP; P03495; 1-70.
DR SMR; Q9Y272; 1-70.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000256; Flu_NS1.
DR Pfam; PF00600; Flu_NS1; 1.
DR ProDom; PD000613; Flu_NS1; 1.
SQ SEQUENCE 230 AA; 26155 MW; 8CCE20E9B572F976 CRC64;

Query Match 99.9%; Score 1177; DB 2; Length 230;
Best Local Similarity 99.6%; Pred. No. 5.8e-91;
Matches 229; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSNTVSSFQVDCFLWHVYKRFADQELGDAFLDLRLRDQKSLKGRGSLGLDIETATRA 60
DB 1 MDSNTVSSFQVDCFLWHVYKRFADQELGDAFLDLRLRDQKSLKGRGSLGLDIETATRA 60
QY 61 GKQIVEQLLEESDEALAKWTIASVPASRYLTDMTLDMSRDWFMFMPKQKVTGSLCIRMD 120
DB 61 GKQIVEQLLEESDEALAKWTIASVPASRYLTDMTLDMSRDWFMFMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIIKANFSVIFERLETLILRAFTGEGAVGVEISPLSPFGHTNEDVKNAIGV 180
DB 121 QAIMDKNIIKANFSVIFERLETLILRAFTGEGAVGVEISPLSPFGHTNEDVKNAIGV 180
QY 181 LIGLKWNDNTVRISETLQRFANRSHENGSRPSFPKQKRWERTIEPEV 230
DB 181 LIGLKWNDNTVRISETLQRFANRSHENGSRPSFPKQKRWERTIEPEV 230

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Db 1 MDSNTVSSFOVDCFLMVRKRFADQELGADPFLDLRRDQSKLGRGSLGLDITETATRA 60
QY 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMTLDEMSRDMFMLMPKQKVTGSLCIRMD 120
Db 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMTLDEMSRDMFMLMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIILKANFSVIFERLETLILLRAFTTEGAVVGEISPLPSLPCHTNEDEVKNAIGV 180
Db 121 QAIMDKNIILKANFSVIFERLETLILLRAFTTEGAVVGEISPLPSLPCHTNEDEVKNAIGV 180
QY 181 LIGGLKWNNTVRISETLQRFARWSSHENGSRPPPKQKRMERTIEPEV 230
Db 181 LIGGLKWNNTVRISETLQRFARWSSHENGSRPPPKQKRMERTIEPEV 230

RESULT 5

QY271_9INFA
ID QY271_9INFA PRELIMINARY; PRT; 230 AA.
AC QY271_9INFA PRELIMINARY; PRT; 230 AA.
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Nonstructural protein NS1.
OS Influenza A virus (A/Equine/Arundel/12369/91 (H3N8)).
OC Viruses; sRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=225093;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98411653; PubMed=9739336; DOI=10.1007/s007050050400;
RA Lindstrom S., Endo A., Sugita S., Pecoraro M., Hiromoto Y., Kamada M.,
RA Takahashi T., Nerome K.;
RT "Phylogenetic analyses of equine influenza M and NS genes and
RT comparison with the HA gene."
RL Arch. Virol. 143:1585-1598(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lindstrom S.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF001669; AAC31260.1; -; Genomic_RNA.
DR HSP; P03495; INS1.
DR SMR; Q9Y271; 1-70.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000256; Flu NS1.
DR Pfam; PF00600; Flu NS1; 1.
DR ProDom; PD000613; Flu NS1; 1.
SQ SEQUENCE 230 AA; 26183 MW; 8DBB20E9A78FC213 CRC64;

Query Match 99.7%; Score 1174; DB 2; Length 230;
Best Local Similarity 99.6%; Pred. No. 1e-90;
Matches 229; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDSNTVSSFOVDCFLMVRKRFADQELGADPFLDLRRDQSKLGRGSLGLDITETATRA 60
Db.. 1 MDSNTVSSFOVDCFLMVRKRFADQELGADPFLDLRRDQSKLGRGSLGLDITETATRA 60
QY 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMTLDEMSRDMFMLMPKQKVTGSLCIRMD 120
Db 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMTLDEMSRDMFMLMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIILKANFSVIFERLETLILLRAFTTEGAVVGEISPLPSLPCHTNEDEVKNAIGV 180
Db 121 QAIMDKNIILKANFSVIFERLETLILLRAFTTEGAVVGEISPLPSLPCHTNEDEVKNAIGV 180
QY 181 LIGGLKWNNTVRISETLQRFARWSSHENGSRPPPKQKRMERTIEPEV 230
Db 181 LIGGLKWNNTVRISETLQRFARWSSHENGSRPPPKQKRMERTIEPEV 230

RESULT 6

QY270_9INFA
ID QY270_9INFA PRELIMINARY; PRT; 230 AA.

AC QY270;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Nonstructural protein NS1.
OS Influenza A virus (A/eq/Roma/5/91 (H3N8)).
OC Viruses; sRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=60023;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98411653; PubMed=9739336; DOI=10.1007/s007050050400;
RA Lindstrom S., Endo A., Sugita S., Pecoraro M., Hiromoto Y., Kamada M.,
RA Takahashi T., Nerome K.;
RT "Phylogenetic analyses of equine influenza M and NS genes and
RT comparison with the HA gene."
RL Arch. Virol. 143:1585-1598(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lindstrom S.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF001669; AAC31262.1; -; Genomic_RNA.
DR HSP; P03495; INS1.
DR SMR; Q9Y270; 1-70.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000256; Flu NS1.
DR Pfam; PF00600; Flu NS1; 1.
DR ProDom; PD000613; Flu NS1; 1.
SQ SEQUENCE 230 AA; 26201 MW; 144DE000EB6851C0 CRC64;
Query Match 99.4%; Score 1171; DB 2; Length 230;
Best Local Similarity 98.7%; Pred. No. 1.9e-90;
Matches 227; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDSNTVSSFOVDCFLMVRKRFADQELGADPFLDLRRDQSKLGRGSLGLDITETATRA 60
Db 1 MDSNTVSSFOVDCFLMVRKRFADQELGADPFLDLRRDQSKLGRGSLGLDITETATRA 60
QY 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMTLDEMSRDMFMLMPKQKVTGSLCIRMD 120
Db 61 GKQIVEQILEESDEALKMTIASVPASRYLTDMTLDEMSRDMFMLMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIILKANFSVIFERLETLILLRAFTTEGAVVGEISPLPSLPCHTNEDEVKNAIGV 180
Db 121 QAIMDKNIILKANFSVIFERLETLILLRAFTTEGAVVGEISPLPSLPCHTNEDEVKNAIGV 180
QY 181 LIGGLKWNNTVRISETLQRFARWSSHENGSRPPPKQKRMERTIEPEV 230
Db 181 LIGGLKWNNTVRISETLQRFARWSSHENGSRPPPKQKRMERTIEPEV 230

RESULT 7

QY275_9INFA
ID QY275_9INFA PRELIMINARY; PRT; 230 AA.
AC QY275;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Nonstructural protein NS1.
OS Influenza A virus (A/eq/Kentucky/1/88 (H3N8)).
OC Viruses; sRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=60030;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98411653; PubMed=9739336; DOI=10.1007/s007050050400;
RA Lindstrom S., Endo A., Sugita S., Pecoraro M., Hiromoto Y., Kamada M.,
RA Takahashi T., Nerome K.;
RT "Phylogenetic analyses of equine influenza M and NS genes and
RT comparison with the HA gene."
RL Arch. Virol. 143:1585-1598(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.

[illegible]


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Q9W9X6_9INFA
ID Q9W9X6_9INFA PRELIMINARY; PRT; 230 AA.
AC Q9W9X6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Nonstructural protein.
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=11320;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98391506; PubMed=9725667; DOI=10.1016/S0168-1702(98)00038-0;
RA Kawaoka Y., Gorman O.T., Ito T., Wells K., Donis R.O., Castrucci M.R.,
RA Donatelli I., Webster R.G.;
RT "Influence of host species on the evolution of the nonstructural (NS)
RT gene of influenza A viruses.";
RL Virus Res. 55:143-156(1998).
DR EMBL; M80976; AAC35584.1; -; Unassigned_RNA.
DR EMBL; M80954; AAC35572.1; -; Unassigned_RNA.
DR HSSP; P03495; 1NS1.
DR SMR; Q9W9X6; 1-70.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000256; Flu NS1.
DR Pfam; PF00600; Flu NS1; 1.
DR ProDom; PD00613; Flu NS1; 1.
DR SEQUENCE 230 AA; 26115 MW; 97CDD1E78490EB5F CRC64;

Query Match 98.4%; Score 1159; DB 2; Length 230;
Best Local Similarity 98.3%; Pred. No. 1.9e-89;
Matches 226; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDSNTVSSFOVDCFLWHVRKRPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60
DB 1 MDSNTVSSFOVDCFLWHVRKRPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60
QY 61 GKQIVEOILEESDEALKWMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
DB 61 GKQIVEOILEESDEALKWMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIILKANFSVIFERLETLILLRAFTGEGAVVGESIPSLPGHTNEDVKNAIGV 180
DB 121 QAIMDKNIILKANFSVIFERLETLILLRAFTGEGAVVGESIPSLPGHTNEDVKNAIGV 180
QY 181 LIQGLKWNNTVRISETLQRFAPWRSSHENGSRPSPPPKQKRMARTIESEV 230
DB 181 LIQGLKWNNTVRISETLQRFAPWRSSHENGSRPSPPPKQKRMARTIESEV 230

RESULT 14
Q9YPE5_9INFA
ID Q9YPE5_9INFA PRELIMINARY; PRT; 230 AA.
AC Q9YPE5;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nonstructural protein.
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=11320;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98391506; PubMed=9725667; DOI=10.1016/S0168-1702(98)00038-0;
RA Kawaoka Y., Gorman O.T., Ito T., Wells K., Donis R.O., Castrucci M.R.,
RA Donatelli I., Webster R.G.;
RT "Influence of host species on the evolution of the nonstructural (NS)
RT gene of influenza A viruses.";
RL Virus Res. 55:143-156(1998).
DR EMBL; M80972; AAC35582.1; -; Unassigned_RNA.
DR HSSP; P03495; 1NS1.
DR SMR; Q9YPE5; 1-70.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000256; Flu NS1.
DR Pfam; PF00600; Flu NS1; 1.
DR ProDom; PD00613; Flu NS1; 1.
DR SEQUENCE 230 AA; 26081 MW; 7723D1178E3AE1FF CRC64;

Query Match 97.9%; Score 1153; DB 2; Length 230;
Best Local Similarity 97.8%; Pred. No. 6.1e-89;
Matches 225; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDSNTVSSFOVDCFLWHVRKRPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60
DB 1 MDSNTVSSFOVDCFLWHVRKRPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60
QY 61 GKQIVEOILEESDEALKWMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
DB 61 GKQIVEOILEESDEALKWMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIILKANFSVIFERLETLILLRAFTGEGAVVGESIPSLPGHTNEDVKNAIGV 180
DB 121 QAIMDKNIILKANFSVIFERLETLILLRAFTGEGAVVGESIPSLPGHTNEDVKNAIGV 180
QY 181 LIQGLKWNNTVRISETLQRFAPWRSSHENGSRPSPPPKQKRMARTIESEV 230
DB 181 LIQGLKWNNTVRISETLQRFAPWRSSHENGSRPSPPPKQKRMARTIESEV 230

RESULT 15
Q9YFD9_9INFA
ID Q9YFD9_9INFA PRELIMINARY; PRT; 230 AA.
AC Q9YFD9;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Nonstructural protein.
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=11320;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98391506; PubMed=9725667; DOI=10.1016/S0168-1702(98)00038-0;
RA Kawaoka Y., Gorman O.T., Ito T., Wells K., Donis R.O., Castrucci M.R.,
RA Donatelli I., Webster R.G.;
RT "Influence of host species on the evolution of the nonstructural (NS)
RT gene of influenza A viruses.";
RL Virus Res. 55:143-156(1998).
DR EMBL; M80972; AAC35582.1; -; Unassigned_RNA.
DR HSSP; P03495; 1NS1.
DR SMR; Q9YFD9; 1-70.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR000256; Flu NS1.
DR Pfam; PF00600; Flu NS1; 1.
DR ProDom; PD00613; Flu NS1; 1.
DR SEQUENCE 230 AA; 26081 MW; 7723D1178E3AE1FF CRC64;

Query Match 97.9%; Score 1153; DB 2; Length 230;
Best Local Similarity 97.8%; Pred. No. 6.1e-89;
Matches 225; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDSNTVSSFOVDCFLWHVRKRPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60
DB 1 MDSNTVSSFOVDCFLWHVRKRPADQELGDAPFLDLRRDQKSLKGRGSLGLDIETATRA 60
QY 61 GKQIVEOILEESDEALKWMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
DB 61 GKQIVEOILEESDEALKWMTIASVPASRYLTDMTLDMSRDWFMMPKQKVTGSLCIRMD 120
QY 121 QAIMDKNIILKANFSVIFERLETLILLRAFTGEGAVVGESIPSLPGHTNEDVKNAIGV 180
DB 121 QAIMDKNIILKANFSVIFERLETLILLRAFTGEGAVVGESIPSLPGHTNEDVKNAIGV 180
QY 181 LIQGLKWNNTVRISETLQRFAPWRSSHENGSRPSPPPKQKRMARTIESEV 230
DB 181 LIQGLKWNNTVRISETLQRFAPWRSSHENGSRPSPPPKQKRMARTIESEV 230
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Db 181 LIGGLKWDNTVRVSETLQRFWRSSHENGRRPFPKQKRMARTIESEV 230

Search completed: March 7, 2006, 19:21:03
Job time : 233 secs

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